

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2003, 04:33:40 ; Search time 114 Seconds
(without alignments)
8668.920 Million cell updates/sec

Title: US-09-667-170A-440
Perfect score: 2239
Sequence: 1 ggaggttgaaagtgcagag.....ttattaaaaaaaaaaaaa 2239

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	366.4	16.4	2072	2	US-09-073-362-2
2	366.4	16.4	2072	2	US-09-243-920-2
3	238.4	10.6	3984	4	US-09-016-434-1199
4	229	10.2	1564	4	US-09-489-847-11
5	211.4	9.4	1011	2	US-08-825-781-2
6	94.2	4.2	1578	4	US-09-107-532A-2089
7	89.2	4.0	1254	4	US-09-107-532A-347
8	67.4	3.0	7218	1	US-08-232-463-14
9	51.6	2.3	62804	4	US-09-800-960-3
10	50	2.2	152331	3	US-09-128-155-16
11	48.6	2.2	148567	4	US-09-801-876B-3
12	47.4	2.1	9862	4	US-09-691-861A-3
13	46.8	2.1	14485	4	US-09-876-216-3
14	44.8	2.0	6124	4	US-08-213-419B-3
15	44.2	2.0	64467	4	US-09-803-671B-3
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17	43.4	1.9	893	4	US-09-370-838-166
18	43.4	1.9	40000	4	US-09-780-049-18
19	43	1.9	83450	4	US-09-811-469-3
20	43	1.9	99500	4	US-09-798-096-10
21	43	1.9	162450	4	US-09-345-882-1
22	42.8	1.9	64467	4	US-09-803-671B-3
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24	42.8	1.9	72604	4	US-09-268-992-7
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					Sequence 1199, Ap
					Sequence 11, Appl
					Sequence 2, Appli
					Sequence 2089, Ap
					Sequence 347, App
					Sequence 14, Appl
					Sequence 3, Appli
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					Sequence 18, Appl
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C 29	42.6	1.9	12047	4	US-09-033-556-3	Sequence 3, Appli
C 30	42.6	1.9	12047	4	US-09-474-699-11	Sequence 11, Appl
C 31	42.4	1.9	3001	4	US-09-539-333D-222	Sequence 22, App
C 32	42.4	1.9	72604	4	US-09-268-992-7	Sequence 7, Appli
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C 34	42.2	1.9	1825	3	US-09-461-697-75	Sequence 75, Appl
C 35	42.2	1.9	7218	1	US-08-232-463-14	Sequence 14, Appl
C 36	42	1.9	83450	4	US-09-811-469-3	Sequence 3, Appli
C 37	41.8	1.9	301	2	US-08-332-766A-23	Sequence 23, Appl
C 38	41.8	1.9	22481	4	US-08-367-841A-43	Sequence 43, Appl
C 39	41.8	1.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl
C 40	41.8	1.9	22484	4	US-09-875-223-2	Sequence 2, Appli
C 41	41.8	1.9	53332	4	US-09-801-861-3	Sequence 3, Appli
C 42	41.6	1.9	55827	4	US-09-813-133A-3	Sequence 3, Appli
C 43	41.4	1.8	471	3	US-09-018-584A-6	Sequence 6, Appli
C 44	41.4	1.8	81001	4	US-09-750-580-1	Sequence 1, Appli
C 45	41.2	1.8	516	3	US-09-018-584A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-073-362-2
; Sequence 2, Application US/09073362
; Patent No. 5942399
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
US-09-073-362-2

Query Match 16.4%; Score 366.4; DB 2; Length 2072;
Best Local Similarity 54.6%; Pred. No. 5.6e-89;

Matches		730;	Conservative	0;	Mismatches	606;	Indels	0;	Gaps	0;
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Db	192	CTCCCTTT	TGGGTGATGGGCCAGCC	CAGGCCGAGCAGGTGA	AGCTGAAGAGGAGAT	251				
QY	360	CACTTT	ACGAGGGAGTCTCCAT	TATCAITGGCACCACAT	CATTGGAGCAGGAATCTTCAT	419				
Db	252	CTCACTGCT	TAAACGGCGTGTCCCTGAT	TGTGGGAACATGATCGGCT	CAGGCATCTTTGT	311				
QY	420	CTCTCCT	TAAGSGGTGTCTCCAGAA	CACGGGAGCGTGGGCAT	GTCTCTGACCACATCTGGAC	479				
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QY	480	GGTGTGT	GGGTCCTGTCTCACTAT	TTTGGAGCTTTGTCTTAT	GCTGAAATGGGAACAACATAT	539				
Db	372	TGTGGGG	GGGCTCTTCTCCGTCTT	TGGGCCCTTGTATGCG	GAATGGGCACCAACAT	431				
QY	540	AAAGAAAT	CTGAGGTCATTAACATAT	ATATTTTGGAAAGTCTTT	TGTGTCATTAACAGCTTT	599				
Db	432	TAAGAAAT	CTGGGCCAGCTATGCCT	ATATCCTGGAGGCCCTTT	TGGAGGANTCCTTGCTTT	491				
QY	600	TGTACGAG	CTGGGTGGAACTCCTCA	TAAATACGCCCTTCAGCT	ACTGTGTGATATCCCT	659				
Db	492	CATCAGAC	CTTGACCTCCCTGCTCAT	CACTATGAGCCACACGAG	CCCATCATTTGCCAT	551				
QY	660	GGCATT	TGGACGCTACATCTCTG	GAACCAATTTTATCAAT	GTGAATCCCTGAACCTTG	719				
Db	552	CACCTTT	GCCTCACTACATGGTAC	AGCCTCTCTTCCGAGCTG	CTTCGCCCTTATGCTGC	611				
QY	720	GATCAAG	CTCATTAACAGCTGTGG	GCATACTGTAGTGATGG	TCTTAAATAGCATGAGTGT	779				
Db	612	CAGCCGC	CTGTGGCTGTGCCTGCA	TTTGTCTTAACTTCACT	TAACTGTGCCTATGT	671				
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Db	732	GGTCATC	GTGGCAGCATTTGTAG	ACTTTGGCCAGGAGCCT	CTACTCATTTTGAGAATC	791				
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Db	792	CTTTGAG	GTTCATCATTTGCACT	TGGTGATGCAATGCCCT	GGCACTGACTCAGCTCTGT	851				
QY	960	TGCATATG	CTGGCTGGTTTACCTC	AACTTTGTACTGAAGA	AGTAGAAAAACCCCTGAAA	1019				
Db	852	CTCCTAC	TCTAGGTGGACACCCCT	CAACTATGTCACTGA	AGAGATCAAGAATCCTGAG	911				
QY	1020	AACCAT	TTCCCTTGCAATATGT	ATATCCATGGCCCAT	TGTCACCATTGGCTATGTG	1079				
Db	912	GAACCTG	CCCTCTCCATTGGCAT	CTCCATGCCCATTTGT	CACCATCTATATCTTGAC	971				
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QY	1140	AGTGAC	CTTTCTGAGCGGCTAC	TGGGAATTTCTCATT	AGCAGTTCCGATCTTTGTGC	1199				
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Db	1092	ATTATC	CTGTTTTGGTGGCCTC	AATGCCCTCATTGTGG	CTGCTTCTAGGCTTTCTTTGT	1151				
QY	1260	TGCGTCT	CGAGAGGTCACCTTCC	CAGAAATCTCTCCAT	GATTCTATGTCGCGAAGCAC	1319				
Db	1152	GGGCTC	AAAGAGAGGCCCATC	TCCCTGATGCGCATCT	GATGATCCATGTTGAGCGGTT	1211				
QY	1320	TCCTCTA	CCAGCTGTTATTTG	TGCACTTTTGACAA	TGATAATGCTCTCTCTGGAGA	1379				
Db	1212	ACCAGT	GCCTTCTCTGCTCTT	CAATGGTATCATGG	CATTGATCTACTTGTGCGTGAAGA	1271				

QY	1380	CCTCGAC	AGTCTTTTGAATTCCT	CAGTTTTCAGGTTG	CCAGGTGGCTTTTAT	TGGGTGGCAGT	1439
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Db	1392	CGTTTCT	TCCCGATTGTCTT	CTGCTCTGCACCAT	CTTCTGTTGGTGT	TCCACTTTA	1451
QY	1560	TTGGA	CCCCATTTAGTACAGG	ATGGCTTCGTCA	TCACTCTGACTGGAG	TCCCTGCCGTA	1619
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QY	1620	TTATCT	CTTTATTATA	1635			
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RESULT 2
US-09-243-920-2
; Sequence 2, Application US/09243920
; Patent No. 5981242
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,920
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/073,362
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
US-09-243-920-2

Query Match 16.4%; Score 366.4; DB 2; Length 2072;
Best Local Similarity 54.6%; Pred. No. 5.6e-89;
Matches 730; Conservative 0; Mismatches 606; Indels 0; Gaps 0;


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57 TCACGGCCGIGAAGTCTACAGCGTGAAGCGCGCCACCCGGTCCAGGATGCTTTTGCCG 116
QY 815 TTTGCAAGCTCAGAGCAATCTGTATAATTATAGTCCCTGGAGTTATGAGCTAATTAAG 874
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
117 CCGCCAAGCTCCTGGCCCTGGCCCTGATCATCTCTGTGGCTTCGTCCAGATCGGGAAG 176
QY 875 GTCAACGCAGAACTT-----TAAAGACGCTTTTCAGGAAGAGATCAAGTATTACGC 928
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177 GTGATGTGTCCATCTAGATCCCAAGTTCATTTGAAGGCACCAAACTGGATGTGGGA 236
QY 929 GGTGGCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACT 988
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237 ACATTGTGCTGGCAATTATACAGCGGCCCTCTTTGCCTATGGAGATGGAATTACTTGAAT 296
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717 TCTTCAACTGGCTCTGCTGGCCCTGGCCATCATCGGCATGATCTGGCTGCGCCACAGAA 776
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QY 1529 CATGCCCTCTTCATGGTTGCCCTTTTCCCTCTATTTCGGACCCATTTTAGTACAGGGATTGGCT 1588
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897 TCACCATCATCTCAGCGGGCTGCCCGTCTACTTCTTCGGGGTCTGTTGGAACCAACAGC 956
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957 CCAAGTGGCT 966
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RESULT 4
US-09-489-847-11
; Sequence 11, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031PI

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; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1564  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-489-847-11  
  
Query Match 10.2%; Score 229; DB 4; Length 1564;  
Best Local Similarity 53.2%; Pred. No. 5.7e-52;  
Matches 484; Conservative 0; Mismatches 425; Indels 0; Gaps 0;  
  
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132 GGAACCCCTGGTACAAAGATATTTTCACTATGTAAAGTATGGCACTGATCGCGTCAATC 191  
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192 GTTGAGGCAATTTGTAGACTTGGCCAGGAGCTCTACTCAATTTGAGAATTCCTTTGAG 251  
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252 GGTTCATCATTTGCAGTGGGTGACATTTGCCCTGGCACTGTACTCAGCTCTGTCTCCTAC 311  
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312 TCAGGCTGGGACACCCCTCAACTATGTCACTGAAGAGATCAAGAATCCTGAGAGGAACCTG 371  
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552 TGTTTGGTGGCCTCAATGCCCTCCATTTGTGGCTGTCTTACGGCTTTTCTTTTGTGGGCTCA 611  
QY 1267 CGAGAGGGTCAACCTTCCAGAAATCCTCTCCATGATTATCTCCGCAAGCACACTCCTCTTA 1326  
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612 AGAGAAGGCCATCTCCCTGATGCCATCTGCATGATCCATGTTGAGCGGTTACACCAAGTG 671  
QY 1327 CCAGCTGTTATTGTTTTCACCCCTTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGAC 1386  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
672 CCTTCTCTGCTCTTCAATGGTATCATGGCATTTGATCTACTTGTGCGTGAAGACATCTTC 731  
QY 1387 AGTCTTTTGAATTTCTCAGTTTTCAGGTTGGCTTTTATTTGAGTGGCAGTTGCTGGG 1446  
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
732 CAGCTCATTAACACTACTACAGCTTCAGCTACTGGTCTTCTTGTGGGGCTTTCTATTGTGGGT 791
```


QY	1447	CTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTTC AAGGTGCCACTGTTTC	1506
Db	792	CAGCTTTATCTGCGCTGGAAGGAGCCTGATCGACCTCGTCCCTCAAGCTCAGCGTTTTC	851
QY	1507	ATCCCAGCTTTGTTTTCCTTACATGCCCTCTTCATGGTTGCCCTTTCCCTCTATTCCGGAC	1566
Db	852	TTCCCGATTGTCTTCTGCTCTGCACCATCTTCCCTGGTGGCTGTCCACCTTACAGTGAT	911
QY	1567	CCATTTAGTACAGGATTGGCTTCGTCAATCACTCTCACTGGAGTCCCTGCGTATTATCTC	1626
Db	912	ACTATCAACTCCCTCATCGGCATTGCCATTGCCCTCTCAGGCCCTGCCCTTTACTTCCTC	971
QY	1627	TTTATTATA	1635
Db	972	ATCATCAGA	980

RESULT 5

US-08-825-781-2
; Sequence 2, Application US/08825781
; Patent No. 5843727
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

Query Match	9.4%	Score 211.4;	DB 2;	Length 1011;
Best Local Similarity	56.3%	Pred. No. 2.6e-47;		
Matches 395;	Conservative	0;	Mismatches 306;	Indels 0;
				Gaps 0;

QY	995	CTGAAGAAGTAGAAAAACCTGAAAAAACCATTCCTCCCTTGCAATATGTATATCCATGGCCA	1054
Db	81	CTGAAGAGATCAAGAAATCCTGAGAGGAACCTGCCCCCTCTCCATTGGCATCTCCATGGCCCA	140
QY	1055	TTGTCAACCATTTGGCTATGTCTGACAAATGTGGCCCTACTTTACGACCATTAAATGCTGAGG	1114
Db	141	TTGTCAACCATCATCTATATCTTGACCAATGTGGCCCTATTATATACTGTGCTAGACATGAGAG	200
QY	1115	AGCTGCTGCTTTTCAAATGCAGTGGCAGTGACCTTTTCTGACGGCTACTGGGAAATTTCT	1174
Db	201	ACATCTTGGCCAGTGATGCTGTGTGACTTTTTCAGATCAGATATTTTGGAAATATTTA	260
QY	1175	CATTAGCAGTTCCGATCTTTTGTGCCCTCTCCTGCTTTGGTCCCATGAACGGTGGTGCT	1234
Db	261	ACTGGATAATCCACTGTCAAGTTGCATTATCCTGTGTTTGGTGGCCTCAATGCCTCCATTG	320
QY	1235	TTGCTGTCTCCAGGTTATTCATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCT	1294
Db	321	TGGCTGCTTCTAGGCTTTTCTTTGTGGGCTCAAGAGAAGGCCATCTCCCTGATGCCATCT	380
QY	1295	CCATGATTCATGTCCGCAAGCACACTCCTCTACACGCTGTTATGTTTTCACACCTTTGA	1354
Db	381	GCATGATCCATGTTGAGCGGTTCAACCCAGTGCCTCTCTGCTCTTCAATGGTATCATGG	440
QY	1355	CAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCCTCAGTTTGGCCA	1414
Db	441	CATTGATCTACTTGTGGGTGGAAGACATCTTCCAGCTCATTAACACTACAGCTTCAGCT	500
QY	1415	GGTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCAG	1474
Db	501	ACTGGTTCTTTGTGGGCTTTCTATTGTGGGTGAGCTTTATCTGCGCTGGAAGGAGCCTG	560
QY	1475	ATATGCATCGTCCCTTTCAAGTGCACACTGTTTCATCCCAGCTTTGTTTTTCTTCACATGCC	1534
Db	561	ATCGACCTCGTCCCCCTCAAGTTCAGCGTTTTTCTTCCGATGTCTTCTGCTCTGACCA	620
QY	1535	TCCTCATGGTTGCCCTTTTCCCTCTATTTCGGACCCATTTAGTACAGGATTTGGCTTCGTCA	1594
Db	621	TCCTCTGGTGGCTGTTCCACTTTACAGTGATACATACTCAACTCCCTCATCGGCATTGCCA	680
QY	1595	TCACTCTGACTGGAGTCCCTGGGTATTATCTCTTTATTATA	1635
Db	681	TTGGCCTCTCAGGCCTGCCCTTTTACTTCTTCATCATCAGA	721

RESULT 6

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US-09-107-532A-2089
; Sequence 2089, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571

```

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/
;
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 2089:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1578 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1578
; SEQUENCE DESCRIPTION: SEQ ID NO: 2089:
US-09-107-532A-2089

Query Match 4.2%; Score 94.2; DB 4; Length 1578;
Best Local Similarity 44.5%; Pred. No. 1.3e-15;
Matches 528; Conservative 0; Mismatches 638; Indels 21; Gaps 3;

QY 327 AGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTAT 386
Db 261 AGTAAAAATAGAAAAATGAATAAAAACGTACGATGGGATTTTACTGCTTTATCGACTGT 320

QY 387 CATTGGCACCATCATTTGGAGCAGGAATCTTCATCTCTCTAAGGCGTGTCCAGAACAC 446
Db 321 TATGGGCACAGTATCGGTGCAGGGGTATTTTTTAAAGCCGCAAGCGTAGCAGAAGTTAC 380

QY 447 GGGCAGCGTGGGCATGCTCTGACCATCTGGACGGTGTGTGGGTCTCTGTCATATTGG 506
Db 381 AGGATCCGCCAGTTTGCATATGTTTCTTGGTTTCTCGGTGGTATGATTTCTGTCTGTC 440

QY 507 AGCTTTGTCTTATGCTGAATTGGGAACAACATAAAGAAATCTGGAGGTCAATTACACATA 566
Db 441 AGGACTAACAGGAGCTGAAGTGGCAGCTGCTATTCAGAAAAACAGGAGGGATGATTAATA 500

QY 567 TATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGTGGAACTCCTCAT 626
Db 501 TATCGAACGGATTTACGGAAATACAGCAGCTTTTATTTGGGTGGCGCAAGTCGTGAT 560

QY 627 AATACGCCCTGCAGTACTGCTGTGATATCCCTGGCAATTTGGACGTACATTCGGAACC 686
Db 561 TTATTTCCAGCAAAATGAGCAGCCTTGTGATCATTTTCGTATACAGTTCGTCATCT 620

QY 687 ATTTTATTCAATGIGAAATCCCTGAACTTGCATCAAGCTCATTACAGCTGTGGGCAT 746
Db 621 ATTTGGTCTTTCCAGTCAAT-----GATTGTTCCCGTAGCTGTACAGCTGC 668

QY 747 AACTGTAGTGATGTTCTTAAATAGCATGAGTGTGAGTGGAGCGCCCGGATCCAGATTTT 806
Db 669 TGTATCGATCCTGTTGTATCAATTTTTAGGTTCTTAAAGCTGGAGGGGCTTTTCAGTCGAT 728

QY 807 CTTAACCTTTTGCAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCT 866
Db 729 TAGCCTTGCTGCAAGCTTATTCCTTTTGTGATCGTCAATTTTCGGTTTGTTCGGACA 788

QY 867 AANTAAAGGTCAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTAC 926
Db 789 AGAAGGAGTAGACTTCCCACTGTTTCCGATCCAAAGCAGGAGAAAACTTTTCATTTTCTC 848

QY 927 GCGGTTGCCACTGGCTTTTATTATGGAATGATGCAATGCTGGCTGGTTTACCTCAA 986
Db 849 AGCCTTGGGAGCGGGCTTGTAGCAACGATGTTTCGCATACGACGGTTGGATACACGTAGG 908
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QY 987 CTTTGTACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTCCTTGCATATGTATATC 1046
Db 909 AATATATTCGGGAGAAATTGAAAAAGCCGGCGAAAGATTTCGCAAAAGCAATTTCTTAGG 968

QY 1047 CATGGCCATTGTCACCACTTGGCTATGTGCTGACAAATGTGGCCCTACTTTACGACCATTA 1106
Db 969 AATCATCGGAATCATGATCGTTTATTATTATTAGTAAATCGGTGTTCTTAAGAACCGCATC 1028

QY 1107 TGCTGAGGAGCTGCTGCTTTTCAAATGCAATGCGAGTGGCAGTGACCTTTTCTAGCGGCTACTGGG 1166
Db 1029 TATCGACGGAGTCGCAGGAAACACAGCAATCGGCAAGTGACGTTGCAAAATGATTTTGG 1088

QY 1167 AAATTTCTCATTAGCAGTTCGGATCTTTTGTGGC---CTCTCCTGCTTTGGCTCCATGAA 1223
Db 1089 CGGCTTCGGTGGAAAGACTGGTCACAGTTGGTATCTTGATTTCTGTTATGGAACCATCAA 1148

QY 1224 CGGTGGTGTGTTTGTCTGTCTCCAGGTTAFTTCTATGTTGCGTCTCGAGAGGTCACCTTCC 1283
Db 1149 TGGCTATACCTTACTGGAATGCGTCTCCCTTATGTTATGGCAAAAGAAAAACAACCTGCC 1208

QY 1284 -----AGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCCTCTACCAGCTGTTAT 1337
Db 1209 TTTTAGCAAGCTCTTTGCTAAACTTCATGATAAAACTAAAGTTCCTGTAGCCGAGGTAT 1268

QY 1338 TGTTTTCACCCCTTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAA 1397
Db 1269 CTTAGAGCTAGTCATCGCTATTGGCATGATGATCGGTGGTGTGATACACTAACGGA 1328

QY 1398 TTTCTCAGTTTTCAGGTTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCT 1457
Db 1329 TATGCTGATCTTTGTCAATTTGGATTTTATACGATGGTCTTTGTTGGTGTCAATTTCT 1388

QY 1458 TCGATACAAATGCCAGATATGCATCGTCTCTTTCCTTTCAAGGTGCCACTGT 1504
Db 1389 TCGTAAAAAAGAACCTGATTTGTTTCGACCATACAAAGTTTCCAATGT 1435

RESULT 7
US-09-107-532A-347
; Sequence 347, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
;
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; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1254 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1254
; SEQUENCE DESCRIPTION: SEQ ID NO: 347:
US-09-107-532A-347

Query Match          4.0%; Score 89.2; DB 4; Length 1254;
Best Local Similarity 44.2%; Pred. No. 2.7e-14;
Matches 523; Conservative 0; Mismatches 638; Indels 21; Gaps 3;

QY 332 GAGAGAAAGTCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTG 391
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 38  GAATGAAAGGCAAACTAAACGAGAAATCAATCTGTTTGGCGCATTAGCTACCGTTATGG 97
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 392 GCACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGTCCAGAACACGGGCA 451
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 98  GAACCGTGATCGGTGCAGGGCTCTTCTTCAAAACTGTCTGTACTGCTAGTACTCAGT 157
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 452 GCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCCCTGTCACTATTGGAGCTT 511
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 512 TGTCTTATGCTGAATTGGGAACAACTATAAAAGAAATCTGGAGTGCATTACACATATATTT 571
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 218 TGACAGTGGCTGAATTAGCTACAGCAATCCCGAAACTGGTGGAGCTGTAAATATATTG 277
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 572 TGGAAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATAATAC 631
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 278 AAGCTGCGTATGGAATAATTGCCAGCTTTTATTAGGATGGCGCAAGCTTGATTACT 337
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 632 GCCCTGCAGCTACTGCTGTGATATCCCTGGCATTCTGGACGCTACATTCTGGAACCAATTT 691
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 338 TTCTGTCTAATATTGCTGCATTATCGATTATCTTTG-----CGACACAAATTGA 385
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 692 TTATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTCAATTACAGCTGTGGGCATAACTG 751
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 386 CGAACTTATTACAATTATCTACCGATTATCTTTTGTGATTGCGATCACCGCTGTTT 445
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 752 TAGTGATGGTCCCTAAATAGCATAGTGTGAGTGTGAGCGCCCGGATCCAGATTTTCTTTAA 811
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 446 CTGTGACAGGGTTGAATTGTTAGGACAAAAAGTCGGTGCTTCTGTACAATCAGTGACGT 505
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 812 CCTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTA 871
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 506 TGATTGTTAAATTAATACCAATTGCTGTGATTGTTCATATGGGGATTATTGACCCAGGAC 565
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 872 AAGGTCAAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTACGCGGT 931
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 566 AAGGAACTGTCCAGTTATTTCCAACTGGAAGCTGGAAGAAGATGTACTTTTGTGCAAGGAT 625
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 932 TGCCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTG 991
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 626 TGAGCAGTGGCTTGTGTAGCAACGGTTGTGCTTATGACGGCTGGTGTGGTGGCAA 685
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 992 TTACTGAAGAAGTAGAAAAACCCCTGAAAAAACCAATCCCTTGGCAATATGTATATCCATGG 1051
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 686 TGGCACGGGAAATGAAACGGCCGGGAAAAAGATTTCCTAAAGCAATTATCTTGGTTTGA 745
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1052 CCATTGTACCATTTGGCTATGTGCTGACAAAATGTGGCCTACTTTACGACCATTAATGCTG 1111
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 746 GTTTTGTAAACAGTCGTTTATCTATTGATCAATTTTGTTTTTTTTGAAAACTTTGCCGATTG 805
Db  ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1112 AGGAGCT--GCTGCTTTCAAATGCAGTGGCAGTGAAGTCTTTCTGAGCGGCTACTGGGAA 1168
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 806 ATCATCTTGCCGGTAATTTGAATGCAGCTTCTGAAGCATCAGACGTCAATTTTGGAGGAA 865
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1169 ATTTCTCATTAGCAGTTCGGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTG 1228
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 866 TCGGTGGAAGCTGGTCACTATTGGGATCTTGAATCTCGGTATACGGTGCATTGAACGGTT 925
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1229 GTGTGTTTGTCTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACTTTCCAGAAA 1288
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 926 ATACACTAACTGGGATCCCGTGCCTTATGCGATGGCTTTAGAAGACGATCTACCTTTCA 985
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1289 TCCTCTCCATGATTCTCGCAAGCACACTCCTCTACCAAGCTGTTATTGTTTTCACACC 1348
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 986 GTAAACAGCTGACAAATCTTTCAAAGAAGTTTACGGTTCCTTATGTCCCTGCGGTTTCC 1045
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1349 CTTTGACAAAT-----GATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCC 1402
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1046 AGTTAGCAGTAGCTTGTATATGATGAGCCTTGGTTCCTTTCGACTTTTAAACACACATGT 1105
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1403 TCAGTTTGGCAGGTGGTCTTTTATTGGGCTGGCAGTGTCTGGGCTGATTATCTTCGAT 1462
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1106 TGATTTTGTGATGTGGCTATTCACTTTACTGATTGTATCGGTGTCTCTATTTTAAACA 1165
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1463 ACAAATGCCAGATATGCAATCGTCTCTTCAAGGTGCCACTGT 1504
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1166 AAAAAGCGCGGAATTGCCAGTCCATATCAAGTACCACTTT 1207
Db  ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 8
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgpt-F1s
US-08-232-463-14

Query Match      3.0%; Score 67.4; DB 1; Length 7218;
Best Local Similarity 2.1%; Pred. No. 4.7e-08;
Matches 8; Conservative 235; Mismatches 136; Indels 0; Gaps 0;

QY 1184 TTCCGATCTTTGTTGCCTCTCCTGCTTTGGTCCATGAACGGTGGTGTGCTGTCT 1243
||| ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1060 TTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1119

QY 1244 CCAGGTTAATCTATGTTGGCTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATC 1303
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1120 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1179

QY 1304 ATGTCGCAAGCACACTCTTACCAGCTGTTTATGTTTTCACCCCTTTGACAATGATAA 1363
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1180 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1239

QY 1364 TGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCTCTCAGTTTGGCAGGTGGCTTT 1423
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1240 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1299

QY 1424 TTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATC 1483
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1300 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1359

QY 1484 GTCCTTTCAAGTGCCACTGTTTCATCCCAGCTTTGTTTTCCTTCCATGCTCTTTCATGG 1543
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1360 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1419

QY 1544 TTGCCCTTTCCCTCTATTTC 1562
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1420 YYYYYYYYYYYYIYGTAC 1438

RESULT 9
US-09-800-960-3/c
; Sequence 3, Application US/098000960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match      2.3%; Score 51.6; DB 4; Length 62804;
Best Local Similarity 70.4%; Pred. No. 0.0024;
Matches 69; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 23 CATGCCAGCTGGGTGACAGTGAGACTCTGTCTCRAACAGAAATTAAGGAAAAAAGAAGA 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43599 CACTCCAGCTGGGTGAGAGTGAGACTCCGTCTAAAAAATAAAAAAATAAAAAAGA 43540

QY 83 AAGAAAAAGAGAGAGAGGAAATTCAGGCCCAATTGTGG 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43539 AAGCAATCTTTTAAGATATCATATTATAGGCCAGGCGTGG 43502
```

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RESULT 10
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match      2.2%; Score 50; DB 3; Length 152331;
Best Local Similarity 73.2%; Pred. No. 0.0098;
Matches 82; Conservative 0; Mismatches 20; Indels 10; Gaps 1;

QY 1 GGAGGTTGAAGTGAGCAGAGATCATG-----CCAGCCTGGGTGACAGTGAGACTC 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151204 GGAGGTTGCAGTGAGCAGAGATCGTGCCACTGCACCTCCAGCCTGGTGACAGGGAGACTC 151263

QY 51 TGCTCAAACAGAAATTAAGGAAAAAAGAAAAAGAAAAAGAAAAAGAGAGAGGAA 102
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151264 CGTCTCAAAAAAATAAAAAACAAAAAACCATAAAAAAACAACAAAAACAA 151315

RESULT 11
US-09-801-876B-3/c
; Sequence 3, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 148567
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(148567)
; OTHER INFORMATION: n = A,T,C or G
US-09-801-876B-3

Query Match      2.2%; Score 48.6; DB 4; Length 148567;
Best Local Similarity 53.1%; Pred. No. 0.023;
Matches 129; Conservative 0; Mismatches 109; Indels 5; Gaps 1;

QY 1 GGAGGTTGAAGTGAGCAGAGATCATGCGCAGCCTGGGTGACAGTGAGACTCTGTCTCAAC 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 79560 GGAGGTTGCAGTGAGCCGAGATCACACCACCTGCACCTCTAGCCTGGGAAACAGAGGGAGAC 79501
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QY 61 AGAATTAAGGAAAAAAGAAAGAAAGAGAGAGAGGAAATTCAGGCC-----AAT 115
Db 79500 TCTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAGAAAGAACCCCTAAAT 79441
QY 116 TGTGGCATAGATTATCATATTCTGGATTTTGTGGATTTCTTTTCTCATCTGG 175
Db 79440 GTTTGCTGTAGTATTTTCACAGTCTGGACTTGGCGATTGCCITTCATGTCACGTCAATCT 79381
QY 176 ATTCAGGAAAGCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTA 235
Db 79380 ATACATTCACAATCTTTGTAGTTTGIAAAAAATTGGTGGTTAGATCTAGAGGCTTGTTT 79321
QY 236 ACG 238
Db 79320 AAG 79318

RESULT 12
US-09-691-861A-3/c
; Sequence 3, Application US/09691861A
; Patent No. 6482935
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000892
; CURRENT APPLICATION NUMBER: US/09/691,861A
; CURRENT FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9862
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-691-861A-3

Query Match 2.1%; Score 47.4; DB 4; Length 9862;
Best Local Similarity 70.8%; Pred. No. 0.013;
Matches 63; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 23 CATGCCAGCCTGGTGACAGTGAGACTCTGTCTCAAAACAGAAATTAAGGAAAAAAGAAAGA 82
Db 4055 CACTCCAGCCTGGGCTAGAGCGGAGACTCTGTCTCAAAAAAAAAAAAAAAAAAAAAAGAA 3996
QY 83 AAGAAAAAGAGAGAGAGGAAATTCAGGC 111
Db 3995 AAGAAAAAAACAGCTAACAGTGTGGC 3967

RESULT 13
US-09-876-216-3/c
; Sequence 3, Application US/09876216
; Patent No. 6544764
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000906
; CURRENT APPLICATION NUMBER: US/09/876,216
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 14485
; TYPE: DNA
; ORGANISM: Human
US-09-876-216-3

Query Match 2.1%; Score 46.8; DB 4; Length 14485;
Best Local Similarity 63.2%; Pred. No. 0.023;

Matches 72; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 23 CATGCCAGCCTGGTGACAGTGAGACTCTGTCTCAAAACAGAAATTAAGGAAAAAAGAAAGA 82
Db 5077 CACTCCAGCCTGGTGACAGAGTGAGACTCTGTCTCTAAAAATAAAATGAAATAAACGA 5018
QY 83 AAGAAAAAGAGAGAGAGGAAATTCAGGCCAAATTTGTGGCATAGATTTTATCATTA 136
Db 5017 TATAAAATAAAATAAGTAAATAACAGGGCAAGGAGACATAAAATGAACAACA 4964

RESULT 14
US-08-213-419B-3/c
; Sequence 3, Application US/08213419B
; Patent No. 6333406
; GENERAL INFORMATION:
; APPLICANT: Inselburg, J. et al.
; TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: JII-002CNC
; CURRENT APPLICATION NUMBER: US/08/213,419B
; CURRENT FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: US 07/870,506
; PRIOR FILING DATE: 1992-04-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2407)..(2439)
; NAME/KEY: CDS
; LOCATION: (2598)..(3404)
; NAME/KEY: CDS
; LOCATION: (3580)..(3720)
; NAME/KEY: CDS
; LOCATION: (3850)..(5835)
US-08-213-419B-3

Query Match 2.0%; Score 44.8; DB 4; Length 6124;
Best Local Similarity 53.4%; Pred. No. 0.054;
Matches 94; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 1788 ATTTTACTTCATTTCTGAAAGTCTAGAGAAATTAACAACCTTGGTGATAAACAAGGAG 1847
Db 2350 ATGTTTGATTATTAAATTTTCTTTATGTTATAATATATATGATTTTATAATATATATAT 2291
QY 1848 TCAGTTATTTTATTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTA 1907
Db 2290 ATATTATTTTATTTTATTTTGGACAATCTAATTAATTTTAAATTTAAATTTT 2231
QY 1908 TAACTCTATGTAGTTATAGAAAAGTGAATATGCAGTTATTTCTATGATCGCACAATT 1963
Db 2230 ATTATATATATATATATAAATTTAATAATAATATATATATATTATTATTAAATTATT 2175

RESULT 15
US-09-803-671B-3/c
; Sequence 3, Application US/09803671B
; Patent No. 6582946
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001161
; CURRENT APPLICATION NUMBER: US/09/803,671B
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3

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; LENGTH: 64467
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(64467)
; OTHER INFORMATION: n = A,T,C or G
US-09-803-671B-3
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Query Match      2.0%; Score 44.2; DB 4; Length 64467;
Best Local Similarity 71.6%; Pred. No. 0.24;
Matches 58; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      23 CATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAACAGAAATTAAGGAAAAAAGAAAGA 82
Db      20865 CACTCCAGCCTGGGTGACAGAGTGAGACCCCTGTCAAAAGAAAGAAAGAAAGAGAGAGA 20806

QY      83 AAGAAAAAGAGAGAGGAGAA 103
Db      20805 GAAAGAGAGAGAGAGAAAAA 20785
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Search completed: October 30, 2003, 07:16:01
Job time : 124 secs
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Db 61 AGAATAAGGAAAAAGAAAAAGAAAAAGAGAGAGAGAAATCCAGGCCCAATTGTGG 120
QY 121 CATAGATTTTATCATATATCTGGATTTTITGGATTCITTTTGTCTCATCATCGGATTCA 180
Db 121 CATAGATTTTATCATATATCTGGATTTTITGGATTCITTTGTCTCATCATCGGATTCA 180
QY 181 GGAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTACCTGCAGGGAAATGTTAACGGG 240
Db 181 GGAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTACCTGCAGGGAAATGTTAACGGG 240
QY 241 AGGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGAGGACGCCCTTTTCAGGAAGAGAC 300
Db 241 AGGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGAGGACGCCCTTTTCAGGAAGAGAC 300
QY 301 GCCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAAGTC 360
Db 301 GCCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAAGTC 360
QY 361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATCATTTGGAGCAGGAATCTTCATC 420
Db 361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATCATTTGGAGCAGGAATCTTCATC 420
QY 421 TCTCCTAAGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 480
Db 421 TCTCCTAAGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 480
QY 481 GTGTGTGGGTCTGTCTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGAAACAACATA 540
Db 481 GTGTGTGGGTCTGTCTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGAAACAACATA 540
QY 541 AAGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATFACCAGCTTTT 600
Db 541 AAGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATFACCAGCTTTT 600
QY 601 GTACGAGTCTGGGTGGAACCTCTCATATAATACGCCCTGCAGTACTGCTGTGATATCCCTG 660
Db 601 GTACGAGTCTGGGTGGAACCTCTCATATAATACGCCCTGCAGTACTGCTGTGATATCCCTG 660
QY 661 GCATTTGGACGCTACATTTCTGGAACCATTTTATTTCAATGTGAATCCCTGAACTTGGC 720
Db 661 GCATTTGGACGCTACATTTCTGGAACCATTTTATTTCAATGTGAATCCCTGAACTTGGC 720
QY 721 ATCAAGCTCATACAGCTGTGGGCATAACTGTAGTGATGGTCCTTAATAGCATGATGTC 780
Db 721 ATCAAGCTCATACAGCTGTGGGCATAACTGTAGTGATGGTCCTTAATAGCATGATGTC 780
QY 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATA 840
Db 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATA 840
QY 841 ATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCC 900
Db 841 ATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCC 900
QY 901 TTTTCAGGAAGAGATTCAGTATTACGGGTTGCCACTGGCTTTTATTTATGGAATGAT 960
Db 901 TTTTCAGGAAGAGATTCAGTATTACGGGTTGCCACTGGCTTTTATTTATGGAATGAT 960
QY 961 GCATATGCTGSGCTGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020
Db 961 GCATATGCTGSGCTGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020
QY 1021 ACCATTCCCTTGCATAATGTATATCCATGSCCATTTGTCAACCATTTGGCTATGTCTGACA 1080
Db 1021 ACCATTCCCTTGCATAATGTATATCCATGSCCATTTGTCAACCATTTGGCTATGTCTGACA 1080
QY 1081 AATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCA 1140
Db 1081 AATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCA 1140
QY 1141 GTGACCTTTTCTGAGCGGCTACTGGGAATTTCTCATTAGCAGTCCGATCTTTTGTGGC 1200

Db 1141 GTGACCTTTTCTGAGCGGCTACTGGGAATTTCTCATTAGCAGTTCGATCTTTTGTGGC 1200
QY 1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGTCTCCAGTTATTTCTATGTT 1260
Db 1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGTCTCCAGTTATTTCTATGTT 1260
QY 1261 GCGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCATGTCGCAAGCACACT 1320
Db 1261 GCGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCATGTCGCAAGCACACT 1320
QY 1321 CCTCTACAGCTGTTATTTGTTTGCACCTTTTGACAATGATAATGCTCTTCTCTGGAGAC 1380
Db 1321 CCTCTACAGCTGTTATTTGTTTGCACCTTTTGACAATGATAATGCTCTTCTCTGGAGAC 1380
QY 1381 CTCGACAGTCTTTTGAATTTCTCTCAGTTTTCAGGTGGCTTTTATTTGGCTGGCAGTT 1440
Db 1381 CTCGACAGTCTTTTGAATTTCTCTCAGTTTTCAGGTGGCTTTTATTTGGCTGGCAGTT 1440
QY 1441 GCTGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCTTCAAGGTGCCA 1500
Db 1441 GCTGGCTGATTTATCTTCGATACAAATGCCCAGATATGCATCGTCTTCAAGGTGCCA 1500
QY 1501 CTGTTCAATCCCAGCTTTTGTCTTCCATGCATGCCCTCTTCATGGTTGCCCTTTCCCTCTAT 1560
Db 1501 CTGTTCAATCCCAGCTTTTGTCTTCCATGCATGCCCTCTTCATGGTTGCCCTTTCCCTCTAT 1560
QY 1561 TCGGACCCATTTAGTACAGGGATTTGGCTTCGTATCACTCTGACTGGAGTCCCTGCGTAT 1620
Db 1561 TCGGACCCATTTAGTACAGGGATTTGGCTTCGTATCACTCTGACTGGAGTCCCTGCGTAT 1620
QY 1621 TATCTCTTTATATATGGGACAAAGAAACCCAGGTGGTTTGAATAAATGTTCAGAGAAAATA 1680
Db 1621 TATCTCTTTATATATGGGACAAAGAAACCCAGGTGGTTTGAATAAATGTTCAGAGAAAATA 1680
QY 1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAGAGATAAAGTTATGAACATAAT 1740
Db 1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCAGAGAGATAAAGTTATGAACATAAT 1740
QY 1741 GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGATTTTACTTTCAT 1800
Db 1741 GGACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGATTTTACTTTCAT 1800
QY 1801 TTTCTGAAAAGTCTAGAGAAATTACAACTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTA 1860
Db 1801 TTTCTGAAAAGTCTAGAGAAATTACAACTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTA 1860
QY 1861 TTCTATATATTTTAGCATATTCGAACTAAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
Db 1861 TTCTATATATTTTAGCATATTCGAACTAAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
QY 1921 TTATAGAAAAGTGAATATGAGTTATTTCTATGAGTCGCAATTTCTTGAGTCTCTGATACC 1980
Db 1921 TTATAGAAAAGTGAATATGAGTTATTTCTATGAGTCGCAATTTCTTGAGTCTCTGATACC 1980
QY 1981 TACCTATTTGGGTTAGGAGAAAAGACTAGACAAATTTACTATGTGGTCAATTTCTTACACAT 2040
Db 1981 TACCTATTTGGGTTAGGAGAAAAGACTAGACAAATTTACTATGTGGTCAATTTCTTACACAT 2040
QY 2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTT 2100
Db 2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTT 2100
QY 2101 TTGTAAGATGGTTTTTACACACTACAGATGCTCTATCTGTGAAAAGTGTTCATTTCTG 2160
Db 2101 TTGTAAGATGGTTTTTACACACTACAGATGCTCTATCTGTGAAAAGTGTTCATTTCTG 2160
QY 2161 AAAAAAGCATACATCATGATTTATGGCAAGAGAGAGAAAGGTAGAGCTGTTCTTAAAT 2220
Db 2161 AAAAAAGCATACATCATGATTTATGGCAAGAGAGAGAAAGGTAGAGCTGTTCTTAAAT 2220
QY 2221 TATTAATAAAAAAAAAAAAAA 2239
Db 2221 TATTAATAAAAAAAAAAAAAA 2239


```
RESULT 2
US-09-854-133-440
; Sequence 440, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 440
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-854-133-440

Query Match      100.0%; Score 2239; DB 10; Length 2239;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGAGGTTGAAGTGACGACAGATCATGCCAGCCTGGGTGACAGTGACAGTGACACTGTGTCTCAAAC 60
Db      1  GGAGGTTGAAGTGACGACAGATCATGCCAGCCTGGGTGACAGTGACAGTGACACTGTGTCTCAAAC 60

QY      61  AGAATTAAGGAAAAAGAAAGAAAGAAAGAGAGAGAGGAAATCCAGGCCAATTGTGG 120
Db      61  AGAATTAAGGAAAAAGAAAGAAAGAAAGAGAGAGAGGAAATCCAGGCCAATTGTGG 120

QY     121  CATAGATTTATCATATTTCTGGATTTTGTGGATTTTGTGGATTTTGTCTCATCACTGGATTCA 180
Db     121  CATAGATTTATCATATTTCTGGATTTTGTGGATTTTGTGGATTTTGTCTCATCACTGGATTCA 180

QY     181  GGAAAGCCTGTGTGTCCACCATCTCCAAAGGAGGTTACCTGCGAGGAAATGTTAACGGG 240
Db     181  GGAAAGCCTGTGTGTCCACCATCTCCAAAGGAGGTTACCTGCGAGGAAATGTTAACGGG 240

QY     241  AGGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCCTTTTCAGGAAGAGAC 300
Db     241  AGGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCCTTTTCAGGAAGAGAC 300

QY     301  GCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCGAGTGAAGAGGAAAGTC 360
Db     301  GCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCGAGTGAAGAGGAAAGTC 360

QY     361  ACTTTACTAGGGGAGTCTCCATTATCATTTGGCACCACCATTTGGAGCAGGAAATCTTCATC 420
Db     361  ACTTTACTAGGGGAGTCTCCATTATCATTTGGCACCACCATTTGGAGCAGGAAATCTTCATC 420

QY     421  TCTCCTAAGGGCGTGTCCAGAACACGGGCAGCGTGGGCATGTCTGTACCATCTGGACG 480
Db     421  TCTCCTAAGGGCGTGTCCAGAACACGGGCAGCGTGGGCATGTCTGTACCATCTGGACG 480

QY     481  GTGTGTGGGTCCTGTCACTATTTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACATA 540
Db     481  GTGTGTGGGTCCTGTCACTATTTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACATA 540

QY     541  AAGAAATCTGGAGGTCATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTT 600
Db     541  AAGAAATCTGGAGGTCATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTT 600

QY     601  GTACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660
Db     601  GTACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660
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QY      661  GCATTTGGACGCTACATTTCTGGAACCACTTTTATTCAATGTGAAATCCCTGAACCTTGGC 720
Db      661  GCATTTGGACGCTACATTTCTGGAACCACTTTTATTCAATGTGAAATCCCTGAACCTTGGC 720

QY     721  ATCAAGCTCATTAACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTC 780
Db     721  ATCAAGCTCATTAACAGCTGTGGGCATAACTGTAGTGATGGTCCTAAATAGCATGAGTGTC 780

QY     781  AGCTGGAGCGCGCGGATCCAGATTTTCTTAACCTTTTGAAGCTCAAGCAATTTCTGATA 840
Db     781  AGCTGGAGCGCGCGGATCCAGATTTTCTTAACCTTTTGAAGCTCAAGCAATTTCTGATA 840

QY     841  ATTATAGTCCCTGGAGTTATGCAGCTAAATAAAGGTCAAAACGCAGAACTTTAAAGACGCC 900
Db     841  ATTATAGTCCCTGGAGTTATGCAGCTAAATAAAGGTCAAAACGCAGAACTTTAAAGACGCC 900

QY     901  TTTTCAGGAAGAGATTCAAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGAT 960
Db     901  TTTTCAGGAAGAGATTCAAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGAT 960

QY     961  GCATATGCTGGCTGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCCTGAAAAA 1020
Db     961  GCATATGCTGGCTGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCCCTGAAAAA 1020

QY    1021  ACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCAACCATGGCTATGTGCTGACA 1080
Db    1021  ACCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCAACCATGGCTATGTGCTGACA 1080

QY    1081  AATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTCTTCAAATGCAGTGGCA 1140
Db    1081  AATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTCTTCAAATGCAGTGGCA 1140

QY    1141  GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTCCGATCTTTGTTGCC 1200
Db    1141  GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTCCGATCTTTGTTGCC 1200

QY    1201  CTCTCCTGCTTTGGCTCCATGAAACGGTGGTGTGTTTGCTGTCTCCAGGTTATTCTATGTT 1260
Db    1201  CTCTCCTGCTTTGGCTCCATGAAACGGTGGTGTGTTTGCTGTCTCCAGGTTATTCTATGTT 1260

QY    1261  GCGTCTCGAGAGGGTCACTTCCAGAAAATCCTCTCCATGATTCATGTCCGCAAGCACACT 1320
Db    1261  GCGTCTCGAGAGGGTCACTTCCAGAAAATCCTCTCCATGATTCATGTCCGCAAGCACACT 1320

QY    1321  CCTTACCAGCTGTTATTGTTGCAACCCCTTTGACAATGATAAATGCTCTTCTCTGGAGAC 1380
Db    1321  CCTTACCAGCTGTTATTGTTGCAACCCCTTTGACAATGATAAATGCTCTTCTCTGGAGAC 1380

QY    1381  CTCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTTGGCTTTTATTGGGCTGGCAGTT 1440
Db    1381  CTCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTTGGCTTTTATTGGGCTGGCAGTT 1440

QY    1441  GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCAATCGTCTTTCAGAGTGCCA 1500
Db    1441  GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCAATCGTCTTTCAGAGTGCCA 1500

QY    1501  CTGTTTCAATCCCAGCTTTGTTTCTTTCACATGSCCTTTCATGGTTGCCCTTCCCTCTAT 1560
Db    1501  CTGTTTCAATCCCAGCTTTGTTTCTTTCACATGSCCTTTCATGGTTGCCCTTCCCTCTAT 1560

QY    1561  TCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTAT 1620
Db    1561  TCGGACCCATTTAGTACAGGGATTGGCTTCGTCATCACTCTGACTGGAGTCCCTGCGTAT 1620

QY    1621  TATCTCTTTTATATGGGACAAGAAACCCAGTGGTTTAGAATAATGTACAGAGAAAAATA 1680
Db    1621  TATCTCTTTTATATGGGACAAGAAACCCAGTGGTTTAGAATAATGTACAGAGAAAAATA 1680

QY    1681  ACCAGAACATTACAAAATAACTGGAAGTTGTACCAGAAAGATAAGTTATGAACATAAT 1740
Db    1681  ACCAGAACATTACAAAATAACTGGAAGTTGTACCAGAAAGATAAGTTATGAACATAAT 1740

QY    1741  GGACTTGAGATCTTGGCAATCTGCCCCAAGGGGAGACACAAAATAGGGATTTTACTTTCAT 1800
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Db 1741 GGAAGGCTGCTGGCAATCTGCCAAGGGGAGACACAAAATAGGGATTTTACTTCAT 1800
QY 1801 TTTCTGAAAGCTAGAGAAATTACAACTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTA 1860
Db 1801 TTTCTGAAAGCTAGAGAAATTACAACTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTA 1860
QY 1861 TTATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAAATCTATGTAG 1920
Db 1861 TTATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAAATCTATGTAG 1920
QY 1921 TTATAGAAAGTGAATATGAGTATTTCTATGAGTCGACAAATTTCTGATATATGAGT 1980
Db 1921 TTATAGAAAGTGAATATGAGTATTTCTATGAGTCGACAAATTTCTGATATATGAGT 1980
QY 1981 TACCTATTGGGTTAGGAGAAAAGACTAGACAAATTAATGAGTATGAGTATGAGTATGAGT 2040
Db 1981 TACCTATTGGGTTAGGAGAAAAGACTAGACAAATTAATGAGTATGAGTATGAGTATGAGT 2040
QY 2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGTT 2100
Db 2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGTT 2100
QY 2101 TTGTAAAGATGGTTTACACACTACAGATGCTATATGAGTGTGAAAGTGTTCATTTCTG 2160
Db 2101 TTGTAAAGATGGTTTACACACTACAGATGCTATATGAGTGTGAAAGTGTTCATTTCTG 2160
QY 2161 AAAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 AAAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2221 TATTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2239
Db 2221 TATTAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2239
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RESULT 3

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US-10-144-649A-440
; Sequence 440, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 440
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-440
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Query Match 100.0%; Score 2239; DB 14; Length 2239;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
Db 1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAC 60

QY 61 AGAATTAAGGAAAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 AGAATTAAGGAAAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

QY 121 CATAGATTTATCATATTTCTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTT 180
Db 121 CATAGATTTATCATATTTCTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTT 180
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Db 121 CATAGATTTATCATATTTCTGGATTTTGGATTTTGGATTTTGGATTTTGGATTTTGGATTT 180
QY 181 GGAAGGCTGTTCTGTCTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAATGTTAAACGGG 240
Db 181 GGAAGGCTGTTCTGTCTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAATGTTAAACGGG 240
QY 241 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAGGACGCGCTTTTCAGGAAGAG 300
Db 241 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAGGACGCGCTTTTCAGGAAGAG 300
QY 301 GCCTTTTTCAGGAAGAGACGCGCTTTTTCAGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 GCCTTTTTCAGGAAGAGAGACGCGCTTTTTCAGGAAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 ACTTTACTGAGGGGAGTCTCCATTTATCATTTGACCATCATTTGGAGCAGGAATCTTCATC 420
Db 361 ACTTTACTGAGGGGAGTCTCCATTTATCATTTGACCATCATTTGGAGCAGGAATCTTCATC 420
QY 421 TCTCCTAAGGCGTCTCCAGAACACGSGCAGCGTGGGCATGTCCTCTGACCATCTGGACG 480
Db 421 TCTCCTAAGGCGTCTCCAGAACACGSGCAGCGTGGGCATGTCCTCTGACCATCTGGACG 480
QY 481 GTGTGTGGGTCCTGTCTCATTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATA 540
Db 481 GTGTGTGGGTCCTGTCTCATTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATA 540
QY 541 AAGAAATCTGGAGGTCATTACATATATTTTGGAAAGTCTTTGGTCCATTAACAGCTTTT 600
Db 541 AAGAAATCTGGAGGTCATTACATATATTTTGGAAAGTCTTTGGTCCATTAACAGCTTTT 600
QY 601 GTACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGTGTATCCCTG 660
Db 601 GTACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGTGTATCCCTG 660
QY 661 GCATTTGGAGCTACATTTCTGGAACCATTTTATTCAATGTGAATCCCTGAACCTTGGC 720
Db 661 GCATTTGGAGCTACATTTCTGGAACCATTTTATTCAATGTGAATCCCTGAACCTTGGC 720
QY 721 ATCAAGCTCATACAGCTGTGGCATAACTGTAGTATGGTCTTAAATAGCATGAGTGTG 780
Db 721 ATCAAGCTCATACAGCTGTGGCATAACTGTAGTATGGTCTTAAATAGCATGAGTGTG 780
QY 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATA 840
Db 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATA 840
QY 841 ATTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGAGAACTTTAAAGACGCC 900
Db 841 ATTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGAGAACTTTAAAGACGCC 900
QY 901 TTTTCAGGAAGAGATTCAGATTTACCGGTTGCCACTGGCTTTTATTATGGAATGTAT 960
Db 901 TTTTCAGGAAGAGATTCAGATTTACCGGTTGCCACTGGCTTTTATTATGGAATGTAT 960
QY 961 GCATATGCTGGCTGGTTTACCTCAACTTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020
Db 961 GCATATGCTGGCTGGTTTACCTCAACTTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020
QY 1021 ACCATTCCCTTGCATATATGATATCCATGGCCATTGTACCATTTGGCTATGTGCTGACA 1080
Db 1021 ACCATTCCCTTGCATATATGATATCCATGGCCATTGTACCATTTGGCTATGTGCTGACA 1080
QY 1081 AATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAAGTGGCA 1140
Db 1081 AATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAAGTGGCA 1140
QY 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1200
Db 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1200
QY 1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTTCTATGTT 1260
Db 1201 CTCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTTCTATGTT 1260
```

QY 1261 GCGTCTCGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCAATGTCGCAAGCACACT 1320
Db |||||
QY 1261 GCGTCTCGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCAATGTCGCAAGCACACT 1320
Db |||||
QY 1321 CCTCTACCAAGCTGTTATTTGTTTGCACCCCTTGACAAATGATAATGCTCTCTCTGGAGAC 1380
Db |||||
QY 1321 CCTCTACCAAGCTGTTATTTGTTTGCACCCCTTGACAAATGATAATGCTCTCTCTGGAGAC 1380
Db |||||
QY 1381 CTCGACAGCTCTTTTGAATTTCCCTCAGATTTGCCAGGTGGCTTTTATATGGGCTGGCAGTT 1440
Db |||||
QY 1381 CTCGACAGCTCTTTTGAATTTCCCTCAGATTTGCCAGGTGGCTTTTATATGGGCTGGCAGTT 1440
Db |||||
QY 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTCAAGGTGCCA 1500
Db |||||
QY 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTCAAGGTGCCA 1500
Db |||||
QY 1501 CTGTTCTATCCAGCTTTGTTTCCCTTCACATGCCTCTTCATGGTTGCCCTTCCCTCTAT 1560
Db |||||
QY 1501 CTGTTCTATCCAGCTTTGTTTCCCTTCACATGCCTCTTCATGGTTGCCCTTCCCTCTAT 1560
Db |||||
QY 1561 TCGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTCTGACTGGAGTCCCTGCGTAT 1620
Db |||||
QY 1561 TCGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTCTGACTGGAGTCCCTGCGTAT 1620
Db |||||
QY 1621 TATCTCTTTATATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATA 1680
Db |||||
QY 1621 TATCTCTTTATATATGGGACAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATA 1680
Db |||||
QY 1681 ACCAGAACATTTACAAATAATACTGGAAGTTGTACCAGAAGATAAGTTATGAACTAAT 1740
Db |||||
QY 1681 ACCAGAACATTTACAAATAATACTGGAAGTTGTACCAGAAGATAAGTTATGAACTAAT 1740
Db |||||
QY 1741 GGACTTGAGATCTTGGAATCTGCCAAGTGGGAGACACAAAATAGGGATTTTACTTTCAT 1800
Db |||||
QY 1741 GGACTTGAGATCTTGGAATCTGCCAAGTGGGAGACACAAAATAGGGATTTTACTTTCAT 1800
Db |||||
QY 1801 TTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAGAGTCAGTTATTTTAA 1860
Db |||||
QY 1801 TTTCTGAAAGTCTAGAGAATTACAACTTTGGTGATAAACAAAGAGTCAGTTATTTTAA 1860
Db |||||
QY 1861 TTCTATATATTTAGCATATTCGAACTTAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
Db |||||
QY 1861 TTCTATATATTTAGCATATTCGAACTTAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
Db |||||
QY 1921 TTATAGAAAGTGAATATGCAGTTATTTCTATGAGTCGCACAATCTTTGAGTCTCTGATAAC 1980
Db |||||
QY 1921 TTATAGAAAGTGAATATGCAGTTATTTCTATGAGTCGCACAATCTTTGAGTCTCTGATAAC 1980
Db |||||
QY 1981 TACCTATTTGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTTCTCTACAACAT 2040
Db |||||
QY 1981 TACCTATTTGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCATTTCTCTACAACAT 2040
Db |||||
QY 2041 ATGTTAGCACGGCAAGAACCTTCAAAATGAAGACTGAGATTTTCTGTATATATGGGTT 2100
Db |||||
QY 2041 ATGTTAGCACGGCAAGAACCTTCAAAATGAAGACTGAGATTTTCTGTATATATGGGTT 2100
Db |||||
QY 2101 TTGTAAGAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTCATTTCTG 2160
Db |||||
QY 2101 TTGTAAGAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTCATTTCTG 2160
Db |||||
QY 2161 AAAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAGGTAGAGCTGTTCTTAAATT 2220
Db |||||
QY 2161 AAAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAGGTAGAGCTGTTCTTAAATT 2220
Db |||||
QY 2221 TATTAAAAA 2239
Db |||||
QY 2221 TATTAAAAA 2239
Db |||||

RESULT 4
US-10-144-649A-740
; Sequence 740, Application US/10144649A

; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 740
; LENGTH: 6080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-740

Query Match 93.0%; Score 2082.8; DB 14; Length 6080;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2148; Conservative 0; Mismatches 2; Indels 54; Gaps 1;

QY 1 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
Db |||||
QY 93 GGAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAAC 152
Db |||||
QY 61 AGAATTAAGGAAAAAGAAAGAAAAAGAGAGAGAGAAATTCAGGCCAATTGTGG 120
Db |||||
QY 153 AGAATTAAGGAAAAAGAAAGAAAAAGAGAGAGAGAAATTCAGGCCAATTGTGG 212
Db |||||
QY 121 CATAGATTTTATCATATTTCTGGATTTTGTGATTTTCTCATCTGATTCATCA 180
Db |||||
QY 213 CATAGATTTTATCATATTTCTGGATTTTGTGATTTTCTCATCTGATTCATCA 272
Db |||||
QY 181 GGAAGCCCTGTTGTCTCCACCATCTCCAAAGAGGTTTACCTGCAGGAAATGTTAACGG 240
Db |||||
QY 273 GGAAGCCCTGTTGTCTCCACCATCTCCAAAGAGGTTTACCTGCAGGAAATGTTAACGG 332
Db |||||
QY 241 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGAGCCCTTTTCAGGAAGAGAC 300
Db |||||
QY 333 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAG- 371
Db |||||
QY 301 GCCTTTTCAGGAAGAGACGCTTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTC 360
Db |||||
QY 372 -----GAGAAAGTGCAGCTGAAGAGGAAAGTC 398
Db |||||
QY 361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCCACCATCATTTGGAGCAGGAATCTTCATC 420
Db |||||
QY 399 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATC 458
Db |||||
QY 421 TCTCCTAAGGGCGTCTCCAGAACACGGGAGCGGTGGGCATGTCTCTGACCATCTGGACG 480
Db |||||
QY 459 TCTCCTAAGGGCGTCTCCAGAACACGGGAGCGGTGGGCATGTCTCTGACCATCTGGACG 518
Db |||||
QY 481 GTGTGTGGGTCTCTCACTATTTGGAGCTTTTGTCTTATGCTGAATTTGGGAACAATA 540
Db |||||
QY 519 GTGTGTGGGTCTCTCACTATTTGGAGCTTTTGTCTTATGCTGAATTTGGGAACAATA 578
Db |||||
QY 541 AAGAAATCTGGAGTCAATTACACATATATTTTGGAGTCTTTGGTCCATTACCAGCTTTT 600
Db |||||
QY 579 AAGAAATCTGGAGTCAATTACACATATATTTTGGAGTCTTTGGTCCATTACCAGCTTTT 638
Db |||||
QY 601 GTACGAGTCTGGGTGAACTCCTCATATAACGCCCTGCAGCTACTGTGTGATATCCCTG 660
Db |||||
QY 639 GTACGAGTCTGGGTGAACTCCTCATATAACGCCCTGCAGCTACTGTGTGATATCCCTG 698
Db |||||
QY 661 GCATTTGGAGCTACATTTCTGGAACCAATTTTATTTCAATGTGAAATCCCTGAACCTTGC 720
Db |||||
QY 699 GCATTTGGAGCTACATTTCTGGAACCAATTTTATTTCAATGTGAAATCCCTGAACCTTGC 758
Db |||||
QY 721 ATCAAGCTCATTACAGCTGTGGGCATAACTGTAGTATGGTCTCTAAATAGCATGAGTGTC 780
Db |||||

QY	183	AAAGCCTGTTGTGCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAAACGGGAG	242
Db	181	AAAGCCTGTTGTGCCACCATCTCCAAAGGAGTTACCTGCAGGGAAATGTTAAACGGGAG	240
QY	243	GCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCCTTTTCAGGAAGAGACGC	302
Db	241	GCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAG-----	277
QY	303	CTTTTTCAGGAAGAGACGCGCTTTTTCAGGAAGAGAGAAAAGTGCAGCTGAAAGAGGAAAGTCAC	362
Db	278	-----GAGAAAGTGCAGCTGAAAGAGGAAAGTCAC	306
QY	363	TTTACTGAGGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTC	422
Db	307	TTTACTGAGGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTC	366
QY	423	TCCTAAGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT	482
Db	367	TCCTAAGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT	426
QY	483	GTGTGGGCTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGAAACAACTATAAA	542
Db	427	GTGTGGGCTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGAAACAACTATAAA	486
QY	543	GAAATCTGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTGT	602
Db	487	GAAATCTGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTGT	546
QY	603	ACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC	662
Db	547	ACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC	606
QY	663	ATTTGGACGCTACATCTCTGGAACCAATTTTATTCAATGTGAAATCCCTGAACTTGGCAT	722
Db	607	ATTTGGACGCTACATCTCTGGAACCAATTTTATTCAATGTGAAATCCCTGAACTTGGCAT	666
QY	723	CAAGCTCATACAGCTGTGGGCATAACTGTAGTGATGGTCTCTAAATAGCATGAGTGTGAG	782
Db	667	CAAGCTCATACAGCTGTGGGCATAACTGTAGTGATGGTCTCTAAATAGCATGAGTGTGAG	726
QY	783	CTGGAGCGCCCGGATCCAGATTTTCTTAAACCTTTTGCAGCTCACAGCAATCTTGATAAT	842
Db	727	CTGGAGCGCCCGGATCCAGATTTTCTTAAACCTTTTGCAGCTCACAGCAATCTTGATAAT	786
QY	843	TATAGTCCCTGGAGTTATGCAGCTAAATPAAAGGTCAAACGCAGAACTTTAAAGACGCCCTT	902
Db	787	TATAGTCCCTGGAGTTATGCAGCTAAATPAAAGGTCAAACGCAGAACTTTAAAGACGCCCTT	846
QY	903	TTCAGGAAGAGATTCAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGATGC	962
Db	847	TTCAGGAAGAGATTCAAGTATTACGGGTTGCCACTGGCTTTTATTATGGAATGATGC	906
QY	963	ATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCCTGAAAAAAC	1022
Db	907	ATATGCTGGCTGGTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAACCCCTGAAAAAAC	966
QY	1023	CATTCCCTTGCATAATGTATATCCATGGCCATTGTCAACCAATTGGCTATGTGCTGACAAA	1082
Db	967	CATTCCCTTGCATAATGTATATCCATGGCCATTGTCAACCAATTGGCTATGTGCTGACAAA	1026
QY	1083	TGTGGCCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGT	1142
Db	1027	TGTGGCCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGT	1086
QY	1143	GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTTGCCCT	1202
Db	1087	GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTTGCCCT	1146
QY	1203	CTCCTGCTTTGGCTCCATGAACGCTGGTGTGTTTGTCTCTCCAGGTTATTCTATGTGC	1262
Db	1147	CTCCTGCTTTGGCTCCATGAACGCTGGTGTGTTTGTCTCTCCAGGTTATTCTATGTGC	1206
QY	1263	GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGAAAGCACACTCC	1322

Db	1207	GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCTCCGCAAGCACACTCC	1266
QY	1323	TCTACCAGCTGTTATTGTTTTCACCCTTTTGACAATGATAATGCTCTCTCTGGAGACCT	1382
Db	1267	TCTACCAGCTGTTATTGTTTTCACCCTTTTGACAATGATAATGCTCTCTCTGGAGACCT	1326
QY	1383	CGACAGTCTTTTGAATTTCCCTCAGTTTTCAGAGGTGGCTTTTATTGGGCTGGCAGTTGC	1442
Db	1327	CGACAGTCTTTTGAATTTCCCTCAGTTTTCAGAGGTGGCTTTTATTGGGCTGGCAGTTGC	1386
QY	1443	TGGGCTGATTTATCTTCGATACAAAATGCCAGATATGCATCGTCTCTTTCAAGGTGCCACT	1502
Db	1387	TGGGCTGATTTATCTTCGATACAAAATGCCAGATATGCATCGTCTCTTTCAAGGTGCCACT	1446
QY	1503	GTTCAATCCCAGCTTTTGTTTTCCCTTCACATGCCCTCTTCATGGTTGCCCTTTCCCTCTATT	1562
Db	1447	GTTCAATCCCAGCTTTTGTTTTCCCTTCACATGCCCTCTTCATGGTTGCCCTTTCCCTCTATT	1506
QY	1563	GGACCCATTTAGTACAGGGAATGGCTTCGTTCATCACCTCGACTGGAGTCCCTGCGTATT	1622
Db	1507	GGACCCATTTAGTACAGGGAATGGCTTCGTTCATCACCTCGACTGGAGTCCCTGCGTATT	1566
QY	1623	TCCTCTTATTATATGGGACAGAAAACCCAGGTGGTTTAGAATAAATGTCAGAGAAAATAAC	1682
Db	1567	TCCTCTTATTATATGGGACAGAAAACCCAGGTGGTTTAGAATAAATGTCAGAGAAAATAAC	1626
QY	1683	CAGAACATTACAAAATAATACTGGAAGTTGTACCAGAGAAGATAAGTTATGAACATAATGG	1742
Db	1627	CAGAACATTACAAAATAATACTGGAAGTTGTACCAGAGAAGATAAGTTATGAACATAATGG	1686
QY	1743	ACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGATTTTACTTTCATTT	1802
Db	1687	ACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAAATAGGGATTTTACTTTCATTT	1746
QY	1803	TCTGAAAGTCTAGAGAAATTACAACTTTGGTGATATAACAAAAGGAGTCAGTTATTTTTATT	1862
Db	1747	TCTGAAAGTCTAGAGAAATTACAACTTTGGTGATATAACAAAAGGAGTCAGTTATTTTTATT	1806
QY	1863	CATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATAGT	1922
Db	1807	CATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATAGT	1866
QY	1923	ATAGAAAGTGAATATGCACTTATTTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACCTA	1982
Db	1867	ATAGAAAGTGAATATGCACTTATTTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACCTA	1926
QY	1983	CCTATTGGGTTAGGAGAAAAAGACTAGACAATTACTATGTGGTCATTTCTCTACAACATAT	2042
Db	1927	CCTATTGGGTTAGGAGAAAAAGACTAGACAATTACTATGTGGTCATTTCTCTACAACATAT	1986
QY	2043	GTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTTCTGTATATATGGGTTTT	2102
Db	1987	GTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTTCTGTATATATGGGTTTT	2046
QY	2103	GTAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTCATTCAGTCTGAA	2162
Db	2047	GTAAGATGGTTTTACACACTACAGATGTCTATACTGTGAAAAGTGTTCATTCAGTCTGAA	2106
QY	2163	AAAAAGCATACATCATGATTATGGCAAGAGGAGAGAAAGGTA	2204
Db	2107	AAAAAGCATACATCATGATTATGGCAAGAGGAGAGAAAGAA	2148

RESULT 6
US-09-854-133-441
; Sequence 441, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.

; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-854-133-441

Query Match 92.9%; Score 2080.8; DB 10; Length 5981;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2146; Conservative 0; Mismatches 2; Indels 54; Gaps 1;

QY 3 AGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAG 62
Db |||||
QY 63 AATTAAGGAAAAAAGAGAAAGAAAAAGAGAGAGAGAAATCCAGGCGCAATTGTGGCA 122
Db |||||
QY 61 AATTAAGGAAAAAAGAGAAAGAAAAAGAGAGAGAGAAATCCAGGCGCAATTGTGGCA 120
Db |||||
QY 123 TAGATTTTATCATATCTCGAATTTTGTGGATCTTTTCTCATCATCTGGATTCAGG 182
Db |||||
QY 121 TAGATTTTATCATATCTCGAATTTTGTGGATCTTTTCTCATCATCTGGATTCAGG 180
Db |||||
QY 183 AAAGCCTGTTGTGCCACCATCTCCAAAGGAGGTACCTGCAGGGAATGTAAACGGGAG 242
Db |||||
QY 181 AAAGCCTGTTGTGCCACCATCTCCAAAGGAGGTACCTGCAGGGAATGTAAACGGGAG 240
Db |||||
QY 243 GCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCCTTTTCAGGAAGAGACGC 302
Db |||||
QY 241 GCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAG-----277
QY 303 CTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCAC 362
Db |||||
QY 278 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCAC 306
QY 363 TTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTC 422
Db |||||
QY 307 TTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTC 366
Db |||||
QY 423 TCCTAAGGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT 482
Db |||||
QY 367 TCCTAAGGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT 426
Db |||||
QY 483 GTGTGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGTCTGAATTTGGGAACAACTATAAA 542
Db |||||
QY 427 GTGTGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGTCTGAATTTGGGAACAACTATAAA 486
Db |||||
QY 543 GAAATCTGGAGTCAATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTTGT 602
Db |||||
QY 487 GAAATCTGGAGTCAATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTTGT 546
Db |||||
QY 603 ACGAGTCTGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC 662
Db |||||
QY 547 ACGAGTCTGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC 606
Db |||||
QY 663 ATTTGGACGCTACATTTCTGGAACCATTTTATTCAATGTGAAATCCCTGAACTTCCGAT 722
Db |||||
QY 607 ATTTGGACGCTACATTTCTGGAACCATTTTATTCAATGTGAAATCCCTGAACTTCCGAT 666
Db |||||
QY 723 CAAGCTCATTAAGCTGTGGGCATAACTGTAGTGATGGTCCCTAAATPAGCATGAGTGCAG 782
Db |||||
QY 667 CAAGCTCATTAAGCTGTGGGCATAACTGTAGTGATGGTCCCTAAATAGCATGAGTGTGAG 726
Db |||||
QY 783 CTGGAGCGCCCGATCCAGATTTTCTTAACCTTTTTCAGAGCTTCAGAGCAATTTCTGATAAT 842
Db |||||
QY 727 CTGGAGCGCCCGATCCAGATTTTCTTAACCTTTTTCAGAGCTTCAGAGCAATTTCTGATAAT 786
Db |||||

QY 843 TATAGTCCCTGGAGTTATGCAGCTAATAATAAGGTCAAAACGCAGAACTTTAAAGACGCCTT 902
Db |||||
QY 787 TATAGTCCCTGGAGTTATGCAGCTAATAATAAGGTCAAAACGCAGAACTTTAAAGACGCCTT 846
Db |||||
QY 903 TTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATATGGAATGTATGC 962
Db |||||
QY 847 TTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATATGGAATGTATGC 906
Db |||||
QY 963 ATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAAAGTAGAAAAACCTGAAAAAAC 1022
Db |||||
QY 907 ATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAAAGTAGAAAAACCTGAAAAAAC 966
Db |||||
QY 1023 CATTCCTCTGCAATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAAA 1082
Db |||||
QY 967 CATTCCTCTGCAATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAAA 1026
Db |||||
QY 1083 TGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTCAAATGCAGTGGCAGT 1142
Db |||||
QY 1027 TGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTCAAATGCAGTGGCAGT 1086
Db |||||
QY 1143 GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCCGATCTTTGTTGCCCT 1202
Db |||||
QY 1087 GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCCGATCTTTGTTGCCCT 1146
Db |||||
QY 1203 CTCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGCTGCCAGGTTATTTCTATGTTGC 1262
Db |||||
QY 1147 CTCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGCTGCCAGGTTATTTCTATGTTGC 1206
Db |||||
QY 1263 GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 1322
Db |||||
QY 1207 GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 1266
Db |||||
QY 1323 TCTACCACTGTTTATGTTTGTGACCCCTTTTGACAATGATAATGCTCTTCTCTGGAGACCT 1382
Db |||||
QY 1267 TCTACCACTGTTTATGTTTGTGACCCCTTTTGACAATGATAATGCTCTTCTCTGGAGACCT 1326
Db |||||
QY 1383 CGACACTCTTTTGAAATTTCCCTCAGTTTTCAGGCTGGCTTTTATTTGGCTGGCAGTTGC 1442
Db |||||
QY 1327 CGACAGTCTTTTGAAATTTCCCTCAGTTTTCAGGCTGGCTTTTATTTGGCTGGCAGTTGC 1386
Db |||||
QY 1443 TGGGCTGATTTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTTCAAGGTGCCACT 1502
Db |||||
QY 1387 TGGGCTGATTTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTTCAAGGTGCCACT 1446
Db |||||
QY 1503 GTTCATCCCAGCTTTGTTTTCCTTCACATGCCCTCTTCATGTTGCCCTTTCCCTCTATTTC 1562
Db |||||
QY 1447 GTTCATCCCAGCTTTGTTTTCCTTCACATGCCCTCTTCATGTTGCCCTTTCCCTCTATTTC 1506
Db |||||
QY 1563 GGACCCATTTAGTACAGGATTTGGCTTCGTCATCACCTCTGACTGGAGTCCCTGCGTATTA 1622
Db |||||
QY 1507 GGACCCATTTAGTACAGGATTTGGCTTCGTCATCACCTCTGACTGGAGTCCCTGCGTATTA 1566
Db |||||
QY 1623 TCTCTTTATTATATGGGACAAAGAAACCCAGGTGGTTTGAATAATGTTCAGAGAAATAAC 1682
Db |||||
QY 1567 TCTCTTTATTATATGGGACAAAGAAACCCAGGTGGTTTGAATAATGTTCAGAGAAATAAC 1626
Db |||||
QY 1683 CAGAACATTACAAATATATCTGGAAGTTGTACCAGAAAGATAGTTATGAACTAATGG 1742
Db |||||
QY 1627 CAGAACATTACAAATATATCTGGAAGTTGTACCAGAAAGATAGTTATGAACTAATGG 1686
Db |||||
QY 1743 ACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTACTTCATTT 1802
Db |||||
QY 1687 ACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTACTTCATTT 1746
Db |||||
QY 1803 TCTGAAAAGTCTAGAGAAATACAACTTTGGTGATAAAACAAAAGGAGTCACTTATTTTATT 1862
Db |||||
QY 1747 TCTGAAAAGTCTAGAGAAATACAACTTTGGTGATAAAACAAAAGGAGTCACTTATTTTATT 1806
Db |||||
QY 1863 CATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTT 1922
Db |||||
QY 1807 CATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTT 1866
Db |||||

QY 1923 ATAGAAAGTGAAATATGCAAGTTATTCTATGAGTCGCAAAATCTTGTAGTCTCTGATACCTA 1982
Db |||||||
1867 ATAGAAAGTGAATATGCAAGTTATTCTATGAGTCGCAAAATCTTGTAGTCTCTGATACCTA 1926
QY 1983 CCTATTGGGTTAGAGAAAAGACTAGACAAATTAATAATGTTGATGTTCTCTACAAACATAT 2042
Db |||||||
1927 CCTATTGGGTTAGAGAAAAGACTAGACAAATTAATAATGTTGATGTTCTCTACAAACATAT 1986
QY 2043 GTTAGCACGGCAAGAACCCTTCAAATTGAAGACTGAGATTTTCTGTATATATGGGTTTT 2102
Db |||||||
1987 GTTAGCACGGCAAGAACCCTTCAAATTGAAGACTGAGATTTTCTGTATATATGGGTTTT 2046
QY 2103 GTAAAGATGTTTACACACTACAGATGTTCTATCTACTGTGAAAAGTGTTCATTTCTGAA 2162
Db |||||||
2047 GTAAAGATGTTTACACACTACAGATGTTCTATCTACTGTGAAAAGTGTTCATTTCAATTCTGAA 2106
QY 2163 AAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAAGGTA 2204
Db |||||||
2107 AAAAAGCATACATCATGATTATGGCAAAGAGGAGAGAAGAA 2148

RESULT 7

US-10-144-649A-441
; Sequence 441, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-441

Query Match 92.9%; Score 2080.8; DB 14; Length 5981;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 2146; Conservative 0; Mismatches 2; Indels 54; Gaps 1;
QY 3 AGGTTGAAGTGACGACGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAG 62
Db |||||||
1 AGGTTGAAGTGACGACGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACAG 60
QY 63 AATTAAGSAAAAAGAAAGAAAGAAAGAGAGAGAGGAAATTCAGGCCAATTGTGGCA 122
Db |||||||
61 AATTAAGSAAAAAGAAAGAAAGAAAGAGAGAGAGGAAATTCAGGCCAATTGTGGCA 120
QY 123 TAGATTTTATCATATTCTGGATTTTGTGGATTTTGTGATTTCTTTTCTCATCACTGGATTTCAGG 182
Db |||||||
121 TAGATTTTATCATATTCTGGATTTTGTGGATTTTGTGATTTCTTTTCTCATCACTGGATTTCAGG 180
QY 183 AAAGCCTGTTGTCCACCATCTCCAAAGGAGGTTTACCTGTCAGGAAATGTTAACGGGAG 242
Db |||||||
181 AAAGCCTGTTGTCTCCACCATCTCCAAAGGAGGTTTACCTGTCAGGAAATGTTAACGGGAG 240
QY 243 GCTGCCTTCCTGGGCAACAAGAGGCCACCTGGGCAGGACGCCCTTTCAGGAAGAGACGC 302
Db |||||||
241 GCTGCCTTCCTGGGCAACAAGAGGCCACCTGGGCAG----- 277
QY 303 CTTTTTCAGGAAGAGACGCCTTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCAC 362
Db |||||||
278 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCAC 306
QY 363 TTTTACTGAGGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTTCATCTC 422

Db |||||||
307 TTTACTGAGGGAGTCTCCATTATCAATTGGCACCATCATTTGGAGCAGGAATCTTTCATCTC 366
QY 423 TCCTAAGGCGTCTCCAGAAACACGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT 482
Db |||||||
367 TCCTAAGGCGTCTCCAGAAACACGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGT 426
QY 483 GTGTGGGTCCTGTCACTATTGTGGAGCTTGTCTTATGCTGAAATGGGAACAACATATAA 542
Db |||||||
427 GTGTGGGTCCTGTCACTATTGTGGAGCTTGTCTTATGCTGAAATGGGAACAACATATAA 486
QY 543 GAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTGT 602
Db |||||||
487 GAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTGT 546
QY 603 ACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC 662
Db |||||||
547 ACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGC 606
QY 663 ATTTGGACGCTACATTTCTGGAAACCATTTTATTCAATGTGAAATCCCTGAACTTGGCAT 722
Db |||||||
607 ATTTGGACGCTACATTTCTGGAAACCATTTTATTCAATGTGAAATCCCTGAACTTGGCAT 666
QY 723 CAAGCTCATTAACAGTGTGGGCAAACTGTAGTGATGGTCCCTAAATAGCATGAGTGTGAG 782
Db |||||||
667 CAAGCTCATTAACAGTGTGGGCAAACTGTAGTGATGGTCCCTAAATAGCATGAGTGTGAG 726
QY 783 CTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATAAT 842
Db |||||||
727 CTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATAAT 786
QY 843 TATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGAGAACTTTTAAAGACGCCTT 902
Db |||||||
787 TATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGAGAACTTTTAAAGACGCCTT 846
QY 903 TTCAGGAAGAGATTCAAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATGC 962
Db |||||||
847 TTCAGGAAGAGATTCAAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATGC 906
QY 963 ATATGCTGGCTGGTTTTTACCTCAACTTTGTACTGAAGAGTAGAAAAACCTGAAAAAAC 1022
Db |||||||
907 ATATGCTGGCTGGTTTTTACCTCAACTTTGTACTGAAGAGTAGAAAAACCTGAAAAAAC 966
QY 1023 CATTCCCTTGCATATGTATATCCATGGCCATTTGTCAACCATTTGGCTATGTGCTGACAAA 1082
Db |||||||
967 CATTCCCTTGCATATGTATATCCATGGCCATTTGTCAACCATTTGGCTATGTGCTGACAAA 1026
QY 1083 TGTGGCCTACTTTTACGACCATTAATGCTGAGGAGCTGTCTCTTTCAAATGCAGTGGCAGT 1142
Db |||||||
1027 TGTGGCCTACTTTTACGACCATTAATGCTGAGGAGCTGTCTCTTTCAAATGCAGTGGCAGT 1086
QY 1143 GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCCGATCTTTGTTGCCCT 1202
Db |||||||
1087 GACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCCGATCTTTGTTGCCCT 1146
QY 1203 CTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTGCTCTCCAGGTTATTCTATGTTGC 1262
Db |||||||
1147 CTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTGCTCTCCAGGTTATTCTATGTTGC 1206
QY 1263 GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 1322
Db |||||||
1207 GTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTCC 1266
QY 1323 TCTACCAGCTGTTATTGTTTGCACCCCTTTTGACAAATGATAATGCTCTTCTCTGAGACCT 1382
Db |||||||
1267 TCTACCAGCTGTTATTGTTTGCACCCCTTTTGACAAATGATAATGCTCTTCTCTGAGACCT 1326
QY 1383 CGACAGTCTTTTGAATTTCCCTCAGTTTTTGGCAGGTGGCTTTTATTGGGCTGGCAGTTGC 1442
Db |||||||
1327 CGACAGTCTTTTGAATTTCCCTCAGTTTTTGGCAGGTGGCTTTTATTGGGCTGGCAGTTGC 1386
QY 1443 TGGGCTGATTTTATCTTCGATACAAATGCCAGATATGTCATCGTCTTTCAAGGTGCCACT 1502
Db |||||||

Db 1387 TGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCTTTCAAGGTGCCACT 1446

QY 1503 GTTCATCCAGCTTTTTCCTTCACATGCCCTCTTCATGGTTGCCCTTCCCTCTATTTC 1562

Db 1447 GTTCATCCAGCTTTTTCCTTCACATGCCCTCTTCATGGTTGCCCTTCCCTCTATTTC 1506

QY 1563 GGACCCATTAGTACAGGANTGGCTTCGTCAATCACTCTGACTGGAGTCCCTGCGTATTA 1622

Db 1507 GGACCCATTAGTACAGGANTGGCTTCGTCACTCTGACTGGAGTCCCTGCGTATTA 1566

QY 1623 TCTCTTTATTATATGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAAC 1682

Db 1567 TCTCTTTATTATATGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAAATAAC 1626

QY 1683 CAGAACATTACAAATAATACTGGAAGTTGTACCCAGAGAAGATAAGTTATGAACATAATGG 1742

Db 1627 CAGAACATTACAAATAATACTGGAAGTTGTACCCAGAGAAGATAAGTTATGAACATAATGG 1686

QY 1743 ACTTGAGATCTTGGCAATCTGCCCAATCTGCCCAAGGGGAGACACAAATAAGGATTTTACTTCATTT 1802

Db 1687 ACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAATAAGGATTTTACTTCATTT 1746

QY 1803 TCTGAAAGCTAGAGAATTACAACTTTGGTGATATAACAAAGGAGTCAGTTATTTTATT 1862

Db 1747 TCTGAAAGCTAGAGAATTACAACTTTGGTGATATAACAAAGGAGTCAGTTATTTTATT 1806

QY 1863 CATATATTTTAGCATATTCGAACTAAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTT 1922

Db 1807 CATATATTTTAGCATATTCGAACTAAATTTCTAAGAAATTTAGTTATAACTCTATGTAGTT 1866

QY 1923 ATAGAAAGTGAATATGCAGTTATTTCTATGAGTCGCACAAATCTTGAGTCTCTGATACCTA 1982

Db 1867 ATAGAAAGTGAATATGCAGTTATTTCTATGAGTCGCACAAATCTTGAGTCTCTGATACCTA 1926

QY 1983 CCTATTGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCAATCTCTACAACATAT 2042

Db 1927 CCTATTGGGTTAGGAGAAAAGACTAGACAATTACTATGTGGTCAATCTCTACAACATAT 1986

QY 2043 GTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTTT 2102

Db 1987 GTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTTT 2046

QY 2103 GTAAAGATGTTTACACACTACAGATGTCATACTGTGAAAAGTGTGTTTCAATTCTGAA 2162

Db 2047 GTAAAGATGTTTACACACTACAGATGTCATACTGTGAAAAGTGTGTTTCAATTCTGAA 2106

QY 2163 AAAAGCATACATCATGATTATGGCAAGAGGAGAGAAGGTA 2204

Db 2107 AAAAGCATACATCATGATTATGGCAAGAGGAGAGAAGAA 2148

RESULT 8

US-10-163-866-31

; Sequence 31, Application US/10163866

; Publication No. US20030027188A1

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-080C

; CURRENT APPLICATION NUMBER: US/10/163,866

; CURRENT FILING DATE: 2002-06-05

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/338,733

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: US 60/357,600

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31

; LENGTH: 3144

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-163-866-31

Query Match 84.9%; Score 1900.2; DB 14; Length 3144;

Best Local Similarity 97.2%; Pred. No. 0;

Mismatches 0; Mismatches 3; Indels 54; Gaps 1;

QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTTACCTGCAGGAAATGTTAACGGGA 241

Db 8 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTTACCTGCAGGAAATGTTAACGGGA 67

QY 242 GGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGAGCGCTTTTCAGGAAGAGACG 301

Db 68 GGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAG----- 105

QY 302 CCTTTTCAGGAAGAGACGCCCTTTTTCAGGAAGAGAGAAAAGTGCAGCTGAAGAGGAAAGTCA 361

Db 106 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCA 133

QY 362 CTTTACTGAGGGGAGTCTCCATTATCATTTGGCACCATCATATTGGAGCAGGAATCTTTCATCT 421

Db 134 CTTTACTGAGGGGAGTCTCCATTATCATTTGGCACCATCATATTGGAGCAGGAATCTTTCATCT 193

QY 422 CTCTTAAGGGCGTGTCTCCAGAACACGGGCGAGCGTGGGCAATGTCTCTGACCATCTGGACGG 481

Db 194 CTCTTAAGGGCGTGTCTCCAGAACACGGGCGAGCGTGGGCAATGTCTCTGACCATCTGGACGG 253

QY 482 TGTGTGGGTCCTGTCACTATTGGAGCTTTGTCTTATGCTGAATTTGGAACTCTTTGGTCCATTACCAGCTTTTG 601

Db 254 TGTGTGGGTCCTGTCACTATTGGAGCTTTGTCTTATGCTGAATTTGGAACTCTTTGGTCCATTACCAGCTTTTG 373

QY 602 TACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGTACTGCTGTGATATCCCTGG 661

Db 374 TACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGTACTGCTGTGATATCCCTGG 433

QY 662 CATTTGGACGCTACATTCITGGAAACCATTTTTTATTCATGCTGAATCCCTGAACTTGGCA 721

Db 434 CATTTGGACGCTACATTCITGGAAACCATTTTTTATTCATGCTGAATCCCTGAACTTGGCA 493

QY 722 TCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGTGCTCTAAATAGCATGAGTGTCA 781

Db 494 TCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGTGCTCTAAATAGCATGAGTGTCA 553

QY 782 GCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATCTGTATAA 841

Db 554 GCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATCTGTATAA 613

QY 842 TTATAGTCCCTGGAGTTATGAGCTAAATTAAGGTCAAAACGAGAACTTTAAAGACGCGCT 901

Db 614 TTATAGTCCCTGGAGTTATGAGCTAAATTAAGGTCAAAACGAGAACTTTAAAGACGCGCT 673

QY 902 TTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTTATGGAATGTATG 961

Db 674 TTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTTATGGAATGTATG 733

QY 962 CATATGCTGGCTGGTTTACCTCAACTTTTGTACTGAAGAGTAGAAAAACCTGAAAAAAA 1021

Db 734 CATATGCTGGCTGGTTTACCTCAACTTTTGTACTGAAGAGTAGAAAAACCTGAAAAAAA 793

QY 1022 CCATTCCCCTTGCATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAA 1081

Db 794 CCATTCCCCTTGCATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAA 853

QY 1082 ATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTTCAATGTCAGTGGCAG 1141

Db 854 ATGTGGCCTACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTTCAATGTCAGTGGCAG 913

QY 1142 TGACCTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTTGCC 1201
Db |||||
914 TGACCTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGGATCTTTGTTGCC 973
QY 1202 TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGTATTCTATGTTG 1261
Db |||||
974 TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGTATTCTATGTTG 1033
QY 1262 CGTCTCGAGAGGCTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACATC 1321
Db |||||
1034 CGTCTCGAGAGGCTCACCTTCCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACATC 1093
QY 1322 CTCTACCACTGTTATTGTTTTCACCCCTTTCACAAATGATAATGCTCTTCTCTGGAGACC 1381
Db |||||
1094 CTCTACCACTGTTATTGTTTTCACCCCTTTCACAAATGATAATGCTCTTCTCTGGAGACC 1153
QY 1382 TCGACAGCTCTTTGAATTCCTCAGTTTTCAGGTGGCTTTTATTGGGCTGGCAGTTG 1441
Db |||||
1154 TCGACAGCTCTTTGAATTCCTCAGTTTTCAGGTGGCTTTTATTGGGCTGGCAGTTG 1213
QY 1442 CTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAGGTGCCAC 1501
Db |||||
1214 CTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAGGTGCCAC 1273
QY 1502 TGTTCACTCCAGCTTTGTTTTCCTTCACATGCCCTCTTCATGTTGCCCTTTCCCTCTATT 1561
Db |||||
1274 TGTTCACTCCAGCTTTGTTTTCCTTCACATGCCCTCTTCATGTTGCCCTTTCCCTCTATT 1333
QY 1562 CGGACCACTTTAGTACAGGGATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT 1621
Db |||||
1334 CGGACCACTTTAGTACAGGGATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT 1393
QY 1622 ATCTCTTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTGAGAGAAATAA 1681
Db |||||
1394 ATCTCTTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTGAGAGAAATAA 1453
QY 1682 CCAGAACATTTACAAATAATCTGGAAGTTGTACCAGAAGAGATAAGTTATGAACATAAG 1741
Db |||||
1454 CCAGAACATTTACAAATAATCTGGAAGTTGTACCAGAAGAGATAAGTTATGAACATAAG 1513
QY 1742 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATPAGGGATTTTACTTTCATT 1801
Db |||||
1514 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATAGGGATTTTACTTTCATT 1573
QY 1802 TTCTGAAAGCTAGAGAAATTACAACTTTGGTGATATAACAAAGAGAGTCAGTTATTTTAT 1861
Db |||||
1574 TTCTGAAAGCTAGAGAAATTACAACTTTGGTGATATAACAAAGAGAGTCAGTTATTTTAT 1633
QY 1862 TCATATATTTTAGCATATTTCGAACATAATTCTAAGAAATTTAGTTATAACTCTATGTAGT 1921
Db |||||
1634 TCATATATTTTAGCATATTTCGAACATAATTCTAAGAAATTTAGTTATAACTCTATGTAGT 1693
QY 1922 TATAGAAAGTGAATATGCGAGTTATTCTATGAGTCGCACAAATCTTGTAGTCTCTGATACCT 1981
Db |||||
1694 TATAGAAAGTGAATATGCGAGTTATTCTATGAGTCGCACAAATCTTGTAGTCTCTGATACCT 1753
QY 1982 ACCTATTGGGTTAGGAGAAAGACTAGACAAATTAATGTTGGTCAATCTCTACACATA 2041
Db |||||
1754 ACCTATTGGGTTAGGAGAAAGACTAGACAAATTAATGTTGGTCAATCTCTACACATA 1813
QY 2042 TGTTAGCACGGCAAGAACCTTCAAATGAAGACTGAGATTTTCTGTATATATGGGTTT 2101
Db |||||
1814 TGTTAGCACGGCAAGAACCTTCAAATGAAGACTGAGATTTTCTGTATATATGGGTTT 1873
QY 2102 TGTAAAGATGGTTTACACACTACAGATGTCTATACTGTGAAAAGTGTCTTCAATTCTGA 2161
Db |||||
1874 TGTAAAGATGGTTTACACACTACAGATGTCTATACTGTGAAAAGTGTCTTCAATTCTGA 1933
QY 2162 AAAAAAGCATACATCATGATTATGGCAAGAGGAGAGAGGTA 2204
Db |||||
1934 AAAAAAGCATACATCATGATTATGGCAAGAGGAGAGAGAGAA 1976

RESULT 9
US-10-163-866-29
; Sequence 29, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-29

Query Match 84.3%; Score 1888.2; DB 14; Length 2482;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1965; Conservative 0; Mismatches 3; Indels 55; Gaps 2;
QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA 241
Db |||||
239 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA 298
QY 242 GGCTGCCTTCCCTGGGCAACAAGGAGGCCACCTGGGCGAGGACGCCTTTTCAGGAAGAGACG 301
Db |||||
299 GGCTGCCTTCCCTGGGCAACAAGGAGGCCACCTGGGCGAG-----GAGAAAGTGACGCTGAAGAGGAAAGTCA 336
QY 302 CCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGACGCTGAAGAGGAAAGTCA 361
Db |||||-----GAGAAAGTGACGCTGAAGAGGAAAGTCA 364
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGACCATCATTTGGAGCAGGAATCTTCATCT 421
Db |||||
365 CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCT 424
QY 422 CTCCTAAGGGCGTGTCTCAGAAACACGGGCGAGCGTGGGCATGTCTGTACCATCTGGACGG 481
Db |||||
425 CTCCTAAGGGCGTGTCTCAGAAACACGGGCGAGCGTGGGCATGTCTGTACCATCTGGACGG 484
QY 482 TGTGTGGGTCTCTGTCACTATTTTGGAGCTTTTGTCTTATGCTGAATTGGGAACTATAA 541
Db |||||
485 TATGTGGGTCTCTGTCACTATTTTGGAGCTTTTGTCTTATGCTGAATTGGGAACTATAA 544
QY 542 AGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACAGCTTTTG 601
Db |||||
545 AGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACAGCTTTTG 604
QY 602 TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGTGTGATATCCCTGG 661
Db |||||
605 TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGTGTGATATCCCTGG 664
QY 662 CATTGGACGCTACATTCTGGAACCATTTTATTCAATGTGAAATCCCTGAACCTTCCGA 721
Db |||||
665 CATTGGACGCTACATTCTGGAACCATTTTATTCAATGTGAAATCCCTGAACCTTCCGA 724
QY 722 TCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGTGGTCTCTAAATAGCATGAGTGTCA 781
Db |||||
725 TCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGTGGTCTCTAAATAGCATGAGTGTCA 784

QY 782 GCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTCGTATAA 841
Db |||||
QY 842 TTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAAACGCAGAACTTTAAAGACGCCT 901
Db |||||
QY 902 TTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATATGGAATGTATG 961
Db |||||
QY 962 CATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAACCCCTGAAAAAA 1021
Db |||||
QY 1022 CCATTTCCCTTGCAAATATGTATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAA 1081
Db |||||
QY 1082 ATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1141
Db |||||
QY 1202 TCTCCTGCTTTGCTCCCATGAACGGTGGTGTTTGTCTGTCTCCAGGTATTCTATGTTG 1261
Db |||||
QY 1262 CGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGCTCCGCAAGCACACTC 1321
Db |||||
QY 1322 CTCTACCAAGCTGTTATGTTTTTGACCCCTTTGCAAAATGATAATGCTCTCTCGAGACC 1381
Db |||||
QY 1382 TCGACAGTCTTTGAATTTCTCTCAGTTTTCAGGTTGGCTTTTATTTGGCTGGCAGTTG 1441
Db |||||
QY 1442 CTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGCTTCAAGGTGCCAC 1501
Db |||||
QY 1502 TGTTTCATCCAGCTTTGTTTTCCCTTCAGATGCCTCTCTCATGGTTGCCCTTTCCCTCTATT 1561
Db |||||
QY 1562 CGGACCCATTTAGTACAGGGATTGGCTTCGTCACTCTGCTGAGTCCCTGCGTATT 1621
Db |||||
QY 1622 ATCTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAAGAAAAATAA 1681
Db |||||
QY 1682 CCAGAACATTACAAAATAACTGGAAGTTGTACCAGAAGAGATAAGTTATGAACATAATG 1741
Db |||||
QY 1742 GACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTACTTTCAAT 1801
Db |||||
QY 1802 TTCTGAAAGTCTAGAGAAATTACAACCTTTGGTGATAAAACAAAAGAGTCAGTTATTTTTAT 1861
Db |||||
QY 1862 TCATATATTTTAGCATATTCGAACATAATTCGAAGAAATTTAGTTATAAATCTATGTAGT 1921

Db 1865 TCATATATTTTAGCATATTCGAACATAATTTCTAAGAAATTTAGTTATAAATCTATGTAGT 1924
QY 1922 TATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACCT 1981
Db 1925 TATAGAAAGTGAATATGCAGTTATTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACCT 1984
QY 1982 ACCTATTGGGGTTAGGAGAAAAAGACTAGACAAATTACTATGTGGTCATTTCTCTACAACATA 2041
Db 2042 TGTTAGCACGGCAAAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTT 2101
QY 2101 TGTTAGCACGGCAAAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTT 2104
Db 2104 TGTTAGCACGGCAAAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTTT 2104
QY 2102 TGTTAAAGATGGTTTTTACACACTACAGATGTCTATCTGCTGAAAAAGTGTTCATTTCAATTTCTGA 2161
Db 2105 TGT-AAGATGGTTTTTACACACTACAGATGTCTATCTGTGAAAAAGTGTTCATTTCAATTTCTGA 2163
QY 2162 AAAAAAGCATACATCATGATTTATGGCAAGAGAGAGAGAGTA 2204
Db 2164 AAAAAAGCATACATCATGATTTATGGCAAGAGAGAGAGAGAA 2206

RESULT 10
US-10-133-013-40
; Sequence 40, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 406992.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1923, 1998, 2026
; OTHER INFORMATION: a, t, c, g, or other
US-10-133-013-40

Query Match 76.6%; Score 1715; DB 12; Length 2041;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 3; Indels 55; Gaps 2;
QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTT-AACGGG 240
Db |||||
QY 241 AGGCTGCCCTTCCTGGCAACAAGGAGCCACCTGGGCGAGGACGCCCTTTTCAGGAAGAGAC 300
Db 248 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAAACGGG 307
QY 308 AGGCTGCCCTTCCTGGCAACAAGGAGCCACCTGGGCAG----- 346
Db 301 GCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTCAGCTGAAGAGAAAGTC 360
Db 347 -----GAGAAAGTCAGCTGAAGAGAAAGTC 373
QY 361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCAATCATTTGGAGCAGGAATCTTCATC 420
Db 374 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATC 433

QY 421 TCTCCTAAGGCGTGTCTCCAGAACACGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 480
Db |||||
434 TCTCCTAAGGCGTGTCTCCAGAACACGGCAGCGTGGGCATGTCTCTGACCATCTGGACG 493
QY 481 GTGTGTGGGTCCTGTGTCACTATTATTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACATA 540
Db |||||
494 GTGTGTGGGTCCTGTGTCACTATTATTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACATA 553
QY 541 AAGAAATCTGGAGGTCATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTT 600
Db |||||
554 AAGAAATCTGGAGGTCATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTT 613
QY 601 GTACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGTGTGATATCCCTG 660
Db |||||
614 GTACGAGTCTGGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGTGTGATATCCCTG 673
QY 661 GCATTTGGACGCTACATTTCTGGAACCAATTTTATTCAATGTGAATCCCTGAACTTGGG 720
Db |||||
674 GCATTTGGACGCTACATTTCTGGAACCAATTTTATTCAATGTGAATCCCTGAACTTGGG 733
QY 721 ATCAAGCTCATTTACAGCTGTGGGCATAACTGTAGTGATGGTCTCTAAATAGCATGAGTGC 780
Db |||||
734 ATCAAGCTCATTTACAGCTGTGGGCATAAATGTAGTGATGGTCTCTAAATAGCATGAGTGC 793
QY 781 AGCTGGACGCCCGGATCCAGATTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATA 840
Db |||||
794 AGCTGGACGCCCGGATCCAGATTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATA 853
QY 841 ATTATAGTCCCTGGAGTTATGCACTAATTAAGGTCAAACGCAGAACTTTAAAGACGCC 900
Db |||||
854 ATTATAGTCCCTGGAGTTATGCACTAATTAAGGTCAAACGCAGAACTTTAAAGACGCC 913
QY 901 TTTTCAGGAAGAGATTCAGTATACGGGTGCGGTTGCCACTGCTTTTATTATGGAATGTAT 960
Db |||||
914 TTTTCAGGAAGAGATTCAGTATACGGGTGCGGTTGCCACTGCTTTTATTATGGAATGTAT 973
QY 961 GCATATGCTGGCTGGTTTTACTCAACTTTGTTACTGAAGAGTAGAAAAACCTTGAAAAA 1020
Db |||||
974 GCATATGCTGGCTGGTTTTACTCAACTTTGTTACTGAAGAGTAGAAAAACCTTGAAAAA 1033
QY 1021 ACCATTCCCCTTGCAATATATATCCATGGCCATTTGCAGCTATGGCTATGGTGTGACA 1080
Db |||||
1034 ACCATTCCCCTTGCAATATATATCCATGGCCATTTGCAGCTATGGCTATGGTGTGACA 1093
QY 1081 AATGTGGCCTACTTTACGACCAATTAATGCTGAGGAGTGTGCTTTTCAAAATGCAAGTCCA 1140
Db |||||
1094 AATGTGGCCTACTTTACGACCAATTAATGCTGAGGAGTGTGCTTTTCAAAATGCAAGTCCA 1153
QY 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTGCC 1200
Db |||||
1154 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTGCC 1213
QY 1201 CTCTCCTGCTTTGGCTCCATGAACGGTGTGTTTGTGTCTCCAGGTTATCTATGTT 1260
Db |||||
1214 CTCTCCTGCTTTGGCTCCATGAACGGTGTGTTTGTGTCTCCAGGTTATCTATGTT 1273
QY 1261 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCGGCAAGCACACT 1320
Db |||||
1274 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCGGCAAGCACACT 1333
QY 1321 CCTCTACCAGCTGTTATTGTTTGGACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGAC 1380
Db |||||
1334 CCTCTACCAGCTGTTATTGTTTGGACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGAC 1393
QY 1381 CTCGACAGTCTTTTGAATTTCTCAGTTTGGCAGTGGCTTTTATTGGGCTGGCAGTT 1440
Db |||||
1394 CTCGACAGTCTTTTGAATTTCTCAGTTTGGCAGTGGCTTTTATTGGGCTGGCAGTT 1453
QY 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGTCATCGTCTTTCAAGGTGCCA 1500
Db |||||
1454 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGTCATCGTCTTTCAAGGTGCCA 1513
QY 1501 CTGTTTCATCCCAGCTTTGTTTTCTTTCATATGCTCTTTCATGTTGGCTTCCCTTCCCTCTAT 1560

Db |||||
1514 CTGTTCATCCCAGCTTTGTTTCCCTTCACATGCCCTTTCATGGTTGCCCTTCCCTCTAT 1573
QY 1561 TCGGACCCATTTAGTACAGGATTTGGCTTCGTCACTACTCTGACTGGAGTCCCTGCGTAT 1620
Db |||||
1574 TCGGACCCATTTAGTACAGGATTTGGCTTCGTCACTACTCTGACTGGAGTCCCTGCGTAT 1633
QY 1621 TATCTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTTCAGAGAAAAATA 1680
Db |||||
1634 TATCTCTTTATTATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTTCAGAGAAAAATA 1693
QY 1681 ACCAGAACATTACAAATAATACTGGAAGTTGTACCCAGAGGAGACACAAAAATAGGATTTTACTTCAAT 1740
Db |||||
1694 ACCAGAACATTACAAATAATACTGGAAGTTGTACCCAGAGGAGACACAAAAATAGGATTTTACTTAAT 1753
QY 1741 GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAAATAGGATTTTACTTCAAT 1800
Db |||||
1754 GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAAATAGGATTTTACTTCAAT 1813
QY 1801 TTTCTGAAAGTCTAGAGAAATTACAACCTTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTATA 1860
Db |||||
1814 TTTCTGAAAGTCTAGAGAAATTACAACCTTTGGTGATAAAACAAAAGGAGTCAGTTATTTTATA 1873
QY 1861 TTCATATATTTTAGCATATTTCGAACTAATTTCTAAGAAATTTAGTTATAAATCTCTATGTAG 1920
Db |||||
1874 TTCATATATTTTAGCATATTTCGAACTAATTTCTAAGAAATTTAGTTATANCTCTATGTAG 1933
QY 1921 TTATAGAAAGTGAATATGCAAGTTATTTATGAGTCGCACAAATTTCTGAGTCTCTGATACC 1980
Db |||||
1934 TTATAGAAAGTGAATATGCAAGTTATTTCTATGAGTCGCACAAATTTCTGAGTCTCTGATACC 1993
QY 1981 TACCTATTGGGTTTAGGAGAAAAAGACTAGACAAATTTACTATGTGGTCAT 2028
Db |||||
1994 TACCNATTGGGTTTAGGAGAAAAAGACTAGACAAATTTACTATGTGGTCAT 2041

RESULT 11

US-10-247-671-78
; Sequence 78, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 78
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 406992.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1923, 1998, 2026
; OTHER INFORMATION: a, t, c, g, or other

US-10-247-671-78
Query Match 76.6%; Score 1715; DB 12; Length 2041;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 1790; Conservative 0; Mismatches 3; Indels 55; Gaps 2;
QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTT-AACGGG 240
Db |||||
248 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAAACGGG 307


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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-30

Query Match      68.8%; Score 1540.8; DB 14; Length 1861;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1606; Conservative 0; Mismatches 2; Indels 54; Gaps 1;

QY 182 GAAAGCCTGTTGTGCCACCATCTCCAAAGGAGGTACCTGCAGGGAATGTTAAACGGGA 241
    |||||
Db 243 GAAAGCCTGTTGTGCCACCATCTCCAAAGGAGGTACCTGCAGGGAATGTTAAACGGGA 302
    |||||

QY 242 GGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGACGCCTTTTTCAGGAAGAGACG 301
    |||||
Db 303 GGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAG----- 340

QY 302 CCTTTTCAGGAAGAGACGCCTTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361
    |||||
Db 341 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCA 368

QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGCAACCATCATTTGGAGCAGGAAATCTTTCATCT 421
    |||||
Db 369 CTTTACTGAGGGAGTCTCCATTATCATTTGGCAACCATCATTTGGAGCAGGAAATCTTTCATCT 428

QY 422 CTCCTAAGGGCTGCTCCAGAAACACGGGACGCTGGGCGCATGCTCTGACCATCTGGACGG 481
    |||||
Db 429 CTCCTAAGGGCTGCTCCAGAAACACGGGACGCTGGGCGCATGCTCTGACCATCTGGACGG 488

QY 482 TGTGTGGGGTCTGTCACTATTATTGGAGCTTTTGTCTTATGCTGAATGGGAACAACATATAA 541
    |||||
Db 489 TGTGTGGGGTCTGTCACTATTATTGGAGCTTTTGTCTTATGCTGAATGGGAACAACATATAA 548

QY 542 AGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTG 601
    |||||
Db 549 AGAAATCTGGAGTCAATTACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTG 608

QY 602 TACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG 661
    |||||
Db 609 TACGAGTCTGGGTGGAACCTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG 668

QY 662 CATTTGGACGCTACATTTCTGGAACCAATTTTATTAATGTAATCCCTGAACTTGCGA 721
    |||||
Db 669 CATTTGGACGCTACATTTCTGGAACCAATTTTATTAATGTAATCCCTGAACTTGCGA 728

QY 722 TCAAGCTCAATTACAGCTGTGGGCATAACTGTAGTATGATGGTCCCTAAATAGCATGAGTGTC 781
    |||||
Db 729 TCAAGCTCAATTACAGCTGTGGGCATAACTGTAGTATGATGGTCCCTAAATAGCATGAGTGTC 788

QY 782 GCTGAGCGCGCGGATCCAGATTTTCTTAACCTTTTGAAGCTCAGCAATTTCTGATAA 841
    |||||
Db 789 GCTGAGCGCGCGGATCCAGATTTTCTTAACCTTTTGAAGCTCAGCAATTTCTGATAA 848

QY 842 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAACGCGAGAACTTTAAAGACGCGCT 901
    |||||
Db 849 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAACGCGAGAACTTTAAAGACGCGCT 908

QY 902 TTTTCAGGAAGAGATTTCAAGTATTACGCGGTTGCCACTGGCTTTTATTTATGGAATGTATG 961
    |||||
Db 909 TTTTCAGGAAGAGATTTCAAGTATTACGCGGTTGCCACTGGCTTTTATTTATGGAATGTATG 968

QY 962 CATATGCTGGCTGGTTTACCTCACTTTGTTACTGAAGAAAGTGAAGAAACCTGAAAAAA 1021
    |||||
Db 969 CATATGCTGGCTGGTTTACCTCACTTTGTTACTGAAGAAAGTGAAGAAACCTGAAAAAA 1028

QY 1022 CCATTCCCTTGCAATATGATATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAA 1081
    |||||
Db 1029 CCATTCCCTTGCAATATGATATATCCATGGCCATTGTCAACCATTTGGCTATGTGCTGACAA 1088

QY 1082 ATGTGGCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1141
    |||||
Db 1089 ATGTGGCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1148

QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTCCGATCTTTGTTGCC 1201
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Db 1149 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTCCGATCTTTGTGCC 1208
    |||||
QY 1202 TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTGTCTCCAGGTTATTTCTATGTTG 1261
    |||||
Db 1209 TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTGTCTCCAGGTTATTTCTATGTTG 1268
    |||||
QY 1262 CGTCTCGAGAGGTCACCTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCACACTC 1321
    |||||
Db 1269 CGTCTCGAGAGGTCACCTTCCAGAAATCTCTCCATGATTCATGTCGCAAGCACACTC 1328
    |||||
QY 1322 CTCTACCCAGCTGTTATTGTTTTTGCACCCCTTTGACAAATGATAATGCTCTTCTGGAGACC 1381
    |||||
Db 1329 CTCTACCCAGCTGTTATTGTTTTTGCACCCCTTTGACAAATGATAATGCTCTTCTGGAGACC 1388
    |||||
QY 1382 TCGACAGTCTTTTGAATTTTCTCAGTTTTGCCAGGTGGCTTTTATTTGGGCTGGCAGTTG 1441
    |||||
Db 1389 TCGACAGTCTTTTGAATTTTCTCAGTTTTGCCAGGTGGCTTTTATTTGGGCTGGCAGTTG 1448
    |||||
QY 1442 CTGGGCTGATTTATCTTCGATACAAATGCCCCAGATATGCATCGTCTTTCAAGGTGCCAC 1501
    |||||
Db 1449 CTGGGCTGATTTATCTTCGATACAAATGCCCCAGATATGCATCGTCTTTCAAGGTGCCAC 1508
    |||||
QY 1502 TGTTCAATCCAGCTTTGTTTTTCCCTTCACATGCCTCTTTTATGTTGGCTTTTCCCTCTATT 1561
    |||||
Db 1509 TGTTCAATCCAGCTTTGTTTTTCCCTTCACATGCCTCTTTTATGTTGGCTTTTCCCTCTATT 1568
    |||||
QY 1562 CGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTCTGACTGGAGTCCCTGCGTATT 1621
    |||||
Db 1569 CGGACCCATTTAGTACAGGATTTGGCTTCGTCTCATCTCTGACTGGAGTCCCTGCGTATT 1628
    |||||
QY 1622 ATCTCTTTATATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAATAA 1681
    |||||
Db 1629 ATCTCTTTATATATGGGACAAGAAACCCAGGTGGTTTAGAATAATGTCAGAGAAATAA 1688
    |||||
QY 1682 CCAGAACATTACAAATAATACTCGAAAGTTGTACCAGAAAGATAAGTTATGAACATAATG 1741
    |||||
Db 1689 CCAGAACATTACAAATAATACTCGAAAGTTGTACCAGAAAGATAAGTTATGAACATAATG 1748
    |||||
QY 1742 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATAGGGATTTTACTTTCATT 1801
    |||||
Db 1749 GACTTGAGATCTTGGCAATCTGCCAAGGGGAGACACAAATAGGGATTTTACTTTCATT 1808
    |||||
QY 1802 TTCTGAAAGTCTAGAGAAATTAACAATTTGGTGATAAACAATAA 1843
    |||||
Db 1809 TTCTGAAAGTCTAGAGAAATTAACAATTTGGTGATAAACAATAA 1850
    |||||

RESULT 13
US-10-163-866-33
; Sequence 33, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1542
; TYPE: DNA
```

; ORGANISM: Homo sapiens
US-10-163-866-33

Query Match 65.0%; Score 1454.4; DB 14; Length 1542;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1519; Conservative 0; Mismatches 1; Indels 54; Gaps 1;

QY 182 GAAAGCCTGTTGTGTCACCACTCTCCAAAGGAGTTACTGTCAGGGAATGTTAAGCGGA 241
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
16 GAAAGCCTGTTGTGTCACCACTCTCCAAAGGAGTTACTGTCAGGGAATGTTAAGCGGA 75
QY 242 GGCCTGCTTCCCTGGGCAACAAGGAGCCACCTGGGCGAGACGCCCTTTTCAGGAAGAGACG 301
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
76 GGCCTGCTTCCCTGGGCAACAAGGAGCCACCTGGGCAG----- 113
QY 302 CTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
114 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCA 141
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCACCATCATTTGGAGCAGGAATCTTCATCT 421
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
142 CTTTACTGAGGGAGTCTCCATTATCATTTGGCACCACCATCATTTGGAGCAGGAATCTTCATCT 201
QY 422 CTCCTAAGGGCGTGCTCCAGAACACGGGCGAGCGTGGGCATGCTCTGACCAATCTGGACGG 481
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
202 CTCCTAAGGGCGTGCTCCAGAACACGGGCGAGCGTGGGCATGCTCTGACCAATCTGGACGG 261
QY 482 TGTGTGGGGTCTCTGTCACTATTTGGAGCTTTTGTCTTATGCTGAATTTGGAAACAATATAA 541
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
262 TGTGTGGGGTCTGTCACTATTTGGAGCTTTTGTCTTATGCTGAATTTGGAAACAATATAA 321
QY 542 AGAAATCTGGAGTCAATACATATATTTTGGAGTCTTTTGGTCCATTACCACTTTTG 601
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
322 AGAAATCTGGAGTCAATACATATATTTTGGAGTCTTTTGGTCCATTACCACTTTTG 381
QY 602 TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGAGCTACTGCTGTGATATCCCTGG 661
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
382 TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGAGCTACTGCTGTGATATCCCTGG 441
QY 662 CATTTGGACGCTACATTTCTGGAACCATTTTTCATCAATGTGAAATCCCTGAACTTGC GA 721
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
442 CATTTGGACGCTACATTTCTGGAACCATTTTTCATCAATGTGAAATCCCTGAACTTGC GA 501
QY 722 TCAAGCTCATTAACAGCTGTGGGCATAACTGTAGTGGTCTCTAAATAGCATGAGTGTC A 781
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
502 TCAAGCTCATTAACAGCTGTGGGCATAACTGTAGTGGTCTCTAAATAGCATGAGTGTC A 561
QY 782 GCTGAGGCGCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATAA 841
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
562 GCTGAGGCGCCGGATCCAGATTTTCTTAACCTTTTGAAGCTCACAGCAATTTCTGATAA 621
QY 842 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAAGCAGAACTTTTAAAGACGCCT 901
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
622 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAAGCAGAACTTTTAAAGACGCCT 681
QY 902 TTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATG 961
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
682 TTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATG 741
QY 962 CATATGCTGGCTGGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAACCCCTGAAAAA 1021
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
742 CATATGCTGGCTGGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAACCCCTGAAAAA 801
QY 1022 CCATTCCCTTGCATATGTATATCCATGGCCATTTTCACCATTTGGCTATGTGCTGACAA 1081
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
802 CCATTCCCTTGCATATGTATATCCATGGCCATTTTCACCATTTGGCTATGTGCTGACAA 861
QY 1082 ATGTGGCCTACTTTACGACCATTAATGTCTGAGAGCTGCTGCTTTTCAATGCAAGTGGCAG 1141
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
862 ATGTGGCCTACTTTACGACCATTAATGTCTGAGAGCTGCTGCTTTTCAATGCAAGTGGCAG 921
QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCAATAGCAGTTCCGATCTTTGTTGCC 1201
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 922 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 981
QY 1202 TCTCCTGCTTTTGGCTCCATGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1261
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
982 TCTCCTGCTTTTGGCTCCATGAACGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1041
QY 1262 CGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCCATGTCGCAAGCACACTC 1321
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1042 CGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCCATGTCGCAAGCACACTC 1101
QY 1322 CTCTACCAAGCTGTTATTTTTCAGAACCTTTGACCAATGATAATGCTCTCTTGGAGACC 1381
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1102 CTCTACCAAGCTGTTATTTTTCAGAACCTTTGACCAATGATAATGCTCTCTTGGAGACC 1161
QY 1382 TCGACAGTCTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTGGGCTGGCAGTTG 1441
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1162 TCGACAGTCTTTGAATTTTCTCAGTTTTCAGAGTGGCTTTTATTGGGCTGGCAGTTG 1221
QY 1442 CTGGGCTGATTATCTTCGATACAAATGCCAGATATGCATCGTCTCTTCAAGGTGCCAC 1501
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1222 CTGGGCTGATTATCTTCGATACAAATGCCAGATATGCATCGTCTCTTCAAGGTGCCAC 1281
QY 1502 TGTTCATCCAGCTTTGTTTTCCTTTCATGCTCTCTCATGGTTGCCCTTTCCCTCTATT 1561
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1282 TGTTCATCCAGCTTTGTTTTCCTTTCATGCTCTCTCATGGTTGCCCTTTCCCTCTATT 1341
QY 1562 CGGACCAATTAGTACAGGATTGGCTTCGTCATCATCTCTGACTGGAGTCCCTGCGTATT 1621
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1342 CGGACCAATTAGTACAGGATTGGCTTCGTCATCATCTCTGACTGGAGTCCCTGCGTATT 1401
QY 1622 ATCTCTTATTATATGGGACAAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAATAA 1681
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1402 ATCTCTTATTATATGGGACAAAGAACCCAGGTGGTTTAGAATAATGTCAGAGAAATAA 1461
QY 1682 CCAGAACATTACAAATAATCTGGAAGTTGTACCAGAAAGATAAGTTATGAACATAATG 1741
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1462 CCAGAACATTACAAATAATCTGGAAGTTGTACCAGAAAGATAAGTTATGAACATAATG 1521
QY 1742 GACTTGAGATCTTG 1755
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1522 GACTTGAGATCTGG 1535

RESULT 14
US-10-163-866-52
; Sequence 52, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-52

Query Match 63.9%; Score 1431.8; DB 14; Length 1528;
Best Local Similarity 96.4%; Pred. No. 0;

Matches 1497; Conservative 0; Mismatches 2; Indels 54; Gaps 1;									
QY	182	GAAGCCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA	241						
Db	30	GAAGCCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA	89						
QY	242	GGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACG	301						
Db	90	GGCTGCCCTCCCTGGGCAACAAGGAGCCACCTGGGCAG	127						
QY	302	CCCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA	361						
Db	128	-----GAGAAAGTGCAGCTGAAGAGGAAAGTCA	155						
QY	362	CTTTACTGAGGGGAGTCTCCATTATATCATTTGGCACCATCATTTGGAGCAGGAATCTTTCATCT	421						
Db	156	CTTTACTGAGGGGAGTCTCCATTATATCATTTGGCACCATCATTTGGAGCAGGAATCTTTCATCT	215						
QY	422	CTCCTAAGGGCGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGG	481						
Db	216	CTCCTAAGGGCGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGG	275						
QY	482	TGTGTGGGTCCTGTCACTATTGGAGCTTTGTCTTTATGTGAATTTGGAAACAACATAAA	541						
Db	276	TGTGTGGGTCCTGTCACTATTGGAGCTTTGTCTTTATGTGAATTTGGAAACAACATAAA	335						
QY	542	AGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTG	601						
Db	336	AGAAATCTGGAGGTCATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTG	395						
QY	602	TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG	661						
Db	396	TACGAGTCTGGGTGGAACCTCCTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG	455						
QY	662	CATTTGGACGCTACATTCTTGGACCATTTTATTCAATGTGAAATCCCTGAACCTTGC	721						
Db	456	CATTTGGACGCTACATTCTTGGACCATTTTATTCAATGTGAAATCCCTGAACCTTGC	515						
QY	722	TCAAGCTCATTACAGCTGTGGGCATACTGTAGTATGTCCTAAATAGCATGAGTGTC	781						
Db	516	TCAAGCTCATTACAGCTGTGGGCATACTGTAGTATGTCCTAAATAGCATGAGTGTC	575						
QY	782	GCTGGAGCGCCCGATCCAGATTTCTTAACCTTTTGCAAGCTCACAGCAATTCAGATAA	841						
Db	576	GCTGGAGCGCCCGATCCAGATTTCTTAACCTTTTGCAAGCTCACAGCAATTCAGATAA	635						
QY	842	TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGAGAACTTTAAAGACGCCT	901						
Db	636	TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGAGAACTTTAAAGACGCCT	695						
QY	902	TTTCAGGAAGAGATTCAAGTATTACCGGTTTGCCACTGGCTTTTATTATGGAATGATG	961						
Db	696	TTTCAGGAAGAGATTCAAGTATTACCGGTTTGCCACTGGCTTTTATTATGGAATGATG	755						
QY	962	CATATGCTGGCTGGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCTGAAAAAA	1021						
Db	756	CATATGCTGGCTGGTTTACCTCAACTTTGTTACTGAAGAAGTAGAAAAACCTGAAAAA	815						
QY	1022	CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCAACATTGGCTATGTGACAAA	1081						
Db	816	CCATTCCCCTTGCAATATGTATATCCATGGCCATTGTCAACATTGGCTATGTGACAAA	875						
QY	1082	ATGTGGCCTACTTTTACGACCAATTAATGCTGAGGAGCTGTGCTTTCAAATGCAGTGGCAG	1141						
Db	876	ATGTGGCCTACTTTTACGACCAATTAATGCTGAGGAGCTGTGCTTTCAAATGCAGTGGCAG	935						
QY	1142	TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCGGATCTTTTGTGCC	1201						
Db	936	TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCGGATCTTTTGTGCC	995						
QY	1202	TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTCTCCAGGTTATTTCTATGTTG	1261						
Db	996	TCTCCTGCTTTGGCTCCATGAACGGTGGTGTGTTTGTCTCTCCAGGTTATTTCTATGTTG	1055						

QY	1262	CGTCTCGAGAGGGTCACCTTCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC	1321						
Db	1056	CGTCTCGAGAGGGTCACCTTCAGAAATCCTCTCCATGATTCATGTCCGCAAGCACACTC	1115						
QY	1322	CTCTACCAGCTGTTATGTTTGCACCCCTTGACAATGATAATGCTCTTCTCTGGAGACC	1381						
Db	1116	CTCTACCAGCTGTTATGTTTGCACCCCTTGACAATGATAATGCTCTTCTCTGGAGACC	1175						
QY	1382	TCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTCAGCTTTTATTTGGGCTGGCAGTTG	1441						
Db	1176	TCGACAGTCTTTTGAATTTCTCAGTTTTCAGGTCAGCTTTTATTTGGGCTGGCAGTTG	1235						
QY	1442	CTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAGGTCGCAC	1501						
Db	1236	CTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTCAGGTCGCAC	1295						
QY	1502	TGTTTCATCCCAGCTTTGTTTCTTTCACATGCCCTTTCATGGTTGCCCTTTCCCTCTATT	1561						
Db	1296	TGTTTCATCCCAGCTTTGTTTCTTTCACATGCCCTTTCATGGTTGCCCTTTCCCTCTATT	1355						
QY	1562	CGGACCCATTTAGTACAGGGATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT	1621						
Db	1356	CGGACCCATTTAGTACAGGGATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT	1415						
QY	1622	ATCTCTTTATTTAGTACAGGGATTGGAGTTCAGAGTTCAGAGAAATGATAAGTTATGA	1681						
Db	1416	ATCTCTTTATTTAGTACAGGGATTGGAGTTCAGAGTTCAGAGAAATGATAAGTTATGA	1475						
QY	1682	CCAGAACATTACAAATAACTGGAAGTTGTACAGAGAAAGATAAGTTATGA	1734						
Db	1476	CCAGAACATTACAAATAACTGGAAGTTGTACAGAGAAAGATAAGTTATGA	1528						

RESULT 15

US-10-163-866-34
; Sequence 34, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-34

Query Match 61.3%; Score 1373.4; DB 14; Length 2000; Best Local Similarity 96.0%; Pred. No. 0; Matches 1441; Conservative 0; Mismatches 6; Indels 54; Gaps 1;									
QY	182	GAAGCCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA	241						
Db	143	GAAGCCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA	202						
QY	242	GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGGACGCCTTTTCAGGAAGAGACG	301						
Db	203	GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAG	240						

QY 302 CCTTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCA 361
Db |||||
241 -----GAGAAAGTGCAGCTGAAGAGGAAAGTCA 268
QY 362 CTTTACTGAGGGAGTCTCCATTATCATTTGGACCATCATTTGGAGCAGGAATCTTTCATCT 421
Db |||||
269 CTTTACTGAGGGAGTCTCCATTATCATTTGGACCATCATTTGGAGCAGGAATCTTTCATCT 328
QY 422 CTCCTAAGGGCGTCTGCCAGAAACACGGGCGAGCTGGGCATGTCTCTGACCATCTGGACGG 481
Db |||||
329 CTCCTAAGGGCGTCTGCCAGAAACACGGGCGAGCTGGGCATGTCTCTGACCATCTGGACGG 388
QY 482 TGTGTGGGGTCCGTGTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACACTATAA 541
Db |||||
389 TGTGTGGGGTCCGTGTCACTATTTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACACTATAA 448
QY 542 AGAAATCTGGAGTCAATACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTG 601
Db |||||
449 AGAAATCTGGAGTCAATACACATATATTTTGGAAAGTCTTTTGGTCCATTACCAGCTTTTG 508
QY 602 TACGAGTCTGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG 661
Db |||||
509 TACGAGTCTGGTGGAACTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGG 568
QY 662 CATTTGGACGCTACATTTCTGGAAACCATTTTATTCAATGTGAATCCCTGAACTTTGCGA 721
Db |||||
569 CATTTGGACGCTACATTTCTGGAAACCATTTTATTCAATGTGAATCCCTGAACTTTGCGA 628
QY 722 TCAAGCTCAATTACAGCTGTGGGCATACTGTAGTGATGGTCCCTAAATAGCATGAGTGTCA 781
Db |||||
629 TCAAGCTCAATTACAGCTGTGGGCATACTGTAGTGATGGTCCCTAAATAGCATGAGTGTCA 688
QY 782 GCTGGAGCGCCCGGATCCAGATTTTCTTAACTTTTGAAGCTCAAGCTCAAGCAATTTCTGATAA 841
Db |||||
689 GCTGGAGCGCCCGGATCCAGATTTTCTTAACTTTTGAAGCTCAAGCTCAAGCAATTTCTGATAA 748
QY 842 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGCAGAACTTTAAAGACGCCT 901
Db |||||
749 TTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAAACGCAGAACTTTAAAGACGCCT 808
QY 902 TTTTCAAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATG 961
Db |||||
809 TTTTCAAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTATG 868
QY 962 CATATGCTGCTGGTGTTTTACCCTCAACTTTGTTTACTGAAGAAAGTAGAAAACCCCTGAAAAA 1021
Db |||||
869 CATATGCTGCTGGTGTTTTACCCTCAACTTTGTTTACTGAAGAAAGTAGAAAACCCCTGAAAAA 928
QY 1022 CCATTCCCTTGCATAATGTATATCCATGGCCATTGTCAACCATTTGCTATGTGCTGACAA 1081
Db |||||
929 CCATTCCCTTGCATAATGTATATCCATGGCCATTGTCAACCATTTGCTATGTGCTGACAA 988
QY 1082 ATGTGGCCCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1141
Db |||||
989 ATGTGGCCCTACTTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAG 1048
QY 1142 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1201
Db |||||
1049 TGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1108
QY 1202 TCTCCTGCTTTGGCTCCATGAACGCTGTGTGTTTGTCTCTCCAGGTTATTCTATGTTG 1261
Db |||||
1109 TCTCCTGCTTTGGCTCCATGAACGCTGTGTGTTTGTCTCTCCAGGTTATTCTATGTTG 1168
QY 1262 CGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCTCCGCAAGCACACTC 1321
Db |||||
1169 CGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTCTCCGCAAGCACACTC 1228
QY 1322 CTCTACCAAGTGTATTGTTTGTGACCCCTTTTGACAAATGATAATGCTCTTCTGAGAGACC 1381
Db |||||
1229 CTCTACCAAGTGTATTGTTTGTGACCCCTTTGACAAATGATAATGCTCTTCTGAGAGACC 1288

QY 1382 TCGACAGTCTTTTGAATTTTCCCTCAGTTTTTCCAGGTGGCTTTTATTGGGCTGGCAGTTG 1441
Db |||||
1289 TCGACAGTCTTTTGAATTTTCCCTCAGTTTTTCCAGGTGGCTTTTATTGGGCTGGCAGTTG 1348
QY 1442 CTGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTTCAAGGTGCCAC 1501
Db |||||
1349 CTGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCCCTTTCAAGGTGCCAC 1408
QY 1502 TGTTTCATCCCAGCTTTGTTTTCTTTCACATGCCTCTTTCATGGTTGCCCTTTTCCCTCTATT 1561
Db |||||
1409 TGTTTCATCCCAGCTTTGTTTTCTTTCACATGCCTCTTTCATGGTTGCCCTTTTCCCTCTATT 1468
QY 1562 CGGACCCATTTTAGTACAGGGAATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT 1621
Db |||||
1469 CGGACCCATTTTAGTACAGGGAATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATT 1528
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Db 1589 C 1589

Search completed: October 30, 2003, 07:34:09
Job time : 1069 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 31, 2003, 10:50:02 ; Search time 38.5 Seconds
(without alignments)
4921.247 Million cell updates/sec

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Perfect score: 4120
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1131.5	27.5	511	2	US-09-073-362-1
4	1131.5	27.5	511	2	US-09-243-920-1
5	741.5	18.0	352	4	US-09-489-847-255
6	730	17.7	370	4	US-09-489-847-127
7	621	15.1	241	2	US-08-825-781-3
8	615	14.9	241	2	US-08-825-781-4
9	537.5	13.0	525	4	US-09-107-532A-5743
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11	475.5	11.5	417	4	US-09-107-532A-4001
12	286	6.9	629	2	US-08-132-990A-8

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14	282.5	6.9	521	4	US-09-134-001C-4290	Sequence 4290, Ap
15	279.5	6.8	622	2	US-08-132-990A-4	Sequence 4, Appli
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17	261	6.3	485	4	US-09-252-991A-32881	Sequence 32881, A
18	259.5	6.3	421	4	US-09-107-532A-4030	Sequence 4030, A
19	257	6.2	484	4	US-09-252-991A-32299	Sequence 32299, A
20	244	5.9	453	4	US-09-328-352-4181	Sequence 4181, Ap
21	237.5	5.8	454	4	US-09-252-991A-30013	Sequence 30013, A
22	237.5	5.8	484	4	US-09-328-352-6041	Sequence 6041, Ap
23	235	5.7	494	4	US-09-328-352-7016	Sequence 7016, Ap
24	232.5	5.6	505	4	US-09-328-352-7155	Sequence 7155, Ap
25	232.5	5.6	672	4	US-09-556-916-26	Sequence 26, Appl
26	232.5	5.6	672	4	US-09-556-916-28	Sequence 28, Appl
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28	231.5	5.6	486	4	US-09-252-991A-31847	Sequence 31847, A
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ALIGNMENTS

RESULT 1
US-09-073-362-3
; Sequence 3, Application US/09073362
; Patent No. 5942399
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166


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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
; US-09-073-362-1

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Percent Similarity:	68.00%	Conservative:	109
Best Local Similarity:	45.05%	Mismatches:	149
Query Match:	27.46%	Indels:	3
DB:	2	Gaps:	2

US-09-667-170A-440 (1-2239) x US-09-073-362-1 (1-511)

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QY 430 GCGTGCTCCAGAACACGCGGACGCTGGGCATGTCTCTGACCATCTGGACGGTGTGGG 489
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RESULT 4

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; Sequence 1, Application US/09243920
; Patent No. 5981242
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

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;
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,920
; FILING DATE:
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/073,362
; FILING DATE:
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; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
; US-09-243-920-1

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Score: 1131.50 Matches: 214
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Best Local Similarity: 45.05% Mismatches: 149
Query Match: 27.46% Indels: 3
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US-09-667-170A-440 (1-2239) x US-09-243-920-1 (1-511)

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RESULT 5
US-09-489-847-255
; Sequence 255, Application US/09489847
; Patent No. 6476195

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 255
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-489-847-255

Alignment Scores:
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Percent Similarity: 66.67%    Conservative: 84
Best Local Similarity: 41.67% Mismatches:    109
Query Match:    18.00%       Indels:       3
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US-09-667-170A-440 (1-2239) x US-09-489-847-255 (1-352)

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QY 1027 CCCCTTGCAATATGATATCATCGGCCATTGTCAACATTGGCTATGTGCTGACAAATGTG 1086
Db 101 ProLeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeuThrAsnVal 120
QY 1087 GCCTACTTTACGACCATTATATGCTGAGGAGCTGCTGCTTTTCAATGCAGTGGCAGTGACC 1146
Db 121 AlaTyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThr 140
QY 1147 TTTTCTGACGGCTACTGGGAATTTCTCATAGCAGTTCGGATCTTTGTTGCCCTCTCC 1206
Db 141 PheAlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerValAlaLeuSer 160
QY 1207 TGCTTTGGCTCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTCTATGTTCGGTCT 1266
Db 161 CysPheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPhePheValGlySer 180
QY 1267 CGAGAGGGTCACTTCCAGAAATCCTCTCCATGATTTCATGTCCGACGACACTCCTCTA 1326
```

```

Db 181 ArgGluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPheThrProVal 200
QY 1327 CCAGCTGTTATTGTTTGCACCCCTTTGACAATGATAATGCTCTTCTCTGGAGACCTCGAC 1386
Db 201 ProSerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePhe 220
QY 1387 AGTCTTTTGAATTTCTCAGTTTTCAGGTTGCCAGGTGGCTTTTATTGGCTGGCAGTTGCTGG 1446
Db 221 GlnLeuIleAsnTyrTyrSerPheSerTyrTrpPhePheValGlyLeuSerIleValGly 240
QY 1447 CTGATTTATCTTCGATACAAATGCCAGATATGTCATCGTCCTTTTCAAGGTGCCACTGTTTC 1506
Db 241 GlnLeuTyrLeuArgTrpLysGluProAspArgProArgProLeuLysLeuSerValPhe 260
QY 1507 ATCCCAGCTTTGTTTTCCTTCACATGCCCTCTTCATGGTTGCCCTTTCCCTCTATTCGGAC 1566
Db 261 PheProIleValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAsp 280
QY 1567 CCATTTAGTACAGGGATGGCTTCGTCACTCATCTGAGTGGAGTCCCTGCGTATTATCTC 1626
Db 281 ThrIleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeu 300
QY 1627 TTTATT-----ATATGGGACAAGAAACCCAGTGGTGTAGATAATAATGTCAGAGAAAAATA 1680
Db 301 IleIleArgValProGluHisLysArgProLeuTyrLeuArgArgIleValGlySerAla 320
QY 1681 ACCAGAACATTACAAATAATA---CTGGAAGTTGTACCAGAGAAGAT 1725
Db 321 ThrArgTyrLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 336

RESULT 6
US-09-489-847-127
; Sequence 127, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (370)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-127

Alignment Scores:
Pred. No.:      6.17e-68      Length:      370
Score:          730.00        Matches:     140
Percent Similarity: 63.76%    Conservative: 87
Best Local Similarity: 39.33% Mismatches:    102
Query Match:    17.72%       Indels:       27
DB:             4           Gaps:         3
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QY 1249 TTATTCTATGTTGGCTCGAGAGGGTCCCTCCAGAAATCCTCTCATGATTCATGTC 1308
Db 83 LeuPhePheValGlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisPro 102
QY 1309 CGCAAGCACACTCCTCTACACAGCTGTTATTGTTTTCACCCCTTTGACAATGATAATGCTC 1368
Db 103 GlnLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeuMetTyrAla 122
QY 1369 TTCTCTGGAGACCTCGACAGCTCTTTTGAATTTCTCAGTTTGGCAGGTGGCTTTTATT 1428
Db 123 PheSerArgAspIlePheSerIleIleAsnPhePheSerPhePheAsnTrpLeuCysVal 142
QY 1429 GGGCTGGCAGTTGCTGGGCTGATTATCTTCGATACAAATGCCAGATATGCTGCTCCT 1488
Db 143 AlaLeuAlaIleIleGlyMetMetTrpLeuArgPheLysLysProGluLeuGluArgPro 162
QY 1489 TTCAGGTGCCACTGTTTCATCCAGCTTTGTTTTCCTTTCACATGCCCTCTTCATGGTTGCC 1548
Db 163 IleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAla 182
QY 1549 CTTTCCCTCTATTCCGACCCATTTAGTACAGGATTTGGCTTCATCCTCTCATCTGACTGGA 1608
Db 183 ValSerPheTrpLysThrProLeuGluCysGlyIleGlyPheAlaIleIleLeuSerGly 202
QY 1609 GTCCTCGCTATTATCTCTTTATTTATATATGGGACAAGAACCCAGGTGGTTTAGAATAATG 1668
Db 203 LeuProValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpIleLeuGlnVal 222
QY 1669 TCAGAGAAAATAACAGAACATTACAAATAATACTGGAAGTTGTACAGAGAA 1722
Db 223 IlePheSerValThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 240

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RESULT 8

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US-08-825-781-4
; Sequence 4, Application US/08825781
; Patent No. 5843727

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GENERAL INFORMATION:

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; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN TUMOR-ASSOCIATED MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

```

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,781
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

```

ATTORNEY/AGENT INFORMATION:

```

; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0262 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

```

INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 181908
US-08-825-781-4

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Alignment Scores:
Pred. No.: 6.22e-56
Score: 615.00
Percent Similarity: 68.07%
Best Local Similarity: 48.32%
Query Match: 14.93%
Indels: 0
Gaps: 2

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US-09-667-170A-440 (1-2239) x US-08-825-781-4 (1-241)

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QY 1009 AACCTGAAAAAACCATTCCTTGCATATATATATCCATGGCCATTGTCACCATTTGGC 1068
Db 3 AsnProTyrArgAsnLeuProLeuAlaIleIleSerLeuProIleValThrLeuVal 22
QY 1069 TATGTGCTGACAAATGTGGCTACTTTACGACCAATTAATGTGAGGAGCTGCTGCTTTCA 1128
Db 23 TyrValLeuThrAsnLeuAlaTyrPheThrThrLeuSerThrGluGlnMetLeuSerSer 42
QY 1129 AATGCAGTGGCAGTACCTTTTCTGACGGCTACTGGGAAATTTCTCATTAGCAGTTCCG 1188
Db 43 GluAlaValAlaValAspPheGlyAsnTyrHisLeuGlyValMetSerTrpIleIlePro 62
QY 1189 ATCTTTGTTGGCTCTCTCTGCTTTTGGCTCCATGAACGGTGGTGTGCTGCTCCAGG 1248
Db 63 ValPheValGlyLeuSerCysPheGlySerValAsnGlySerLeuPheThrSerSerArg 82
QY 1249 TTATTCTATGTTGGCTCTCGAGAGGGTCCACTTCCAGAAATCCTCTCCATGATTCATGTC 1308
Db 83 LeuPhePheValGlySerArgGluGlyHisLeuProSerIleLeuSerMetIleHisPro 102
QY 1309 CGCAAGCACACTCCTCTACACAGCTGTTATTGTTTTCACCCCTTTGACAATGATAATGCTC 1368
Db 103 GlnLeuLeuThrProValProSerLeuValPheThrCysValMetThrLeuLeuTyrAla 122
QY 1369 TTCTCTGGAGACCTCGACAGCTCTTTTGAATTTCTCAGTTTGGCAGGTGGCTTTTATT 1428
Db 123 PheSerLysAspIlePheSerValIleAsnPhePheSerPhePheAsnTrpLeuCysVal 142
QY 1429 GGGCTGGCAGTTGCTGGGCTGATTATCTTCGATACAAATGCCAGATATGCTGCTCCT 1488
Db 143 AlaLeuAlaIleIleGlyMetIleTrpLeuArgHisArgLysProGluLeuGluArgPro 162
QY 1489 TTCAGGTGCCACTGTTTCATCCAGCTTTTCTTCTTCTTCATGCTTTCATGTTGCC 1548
Db 163 IleLysValAsnLeuAlaLeuProValPhePheIleLeuAlaCysLeuPheLeuIleAla 182
QY 1549 CTTTCCCTCTATTCCGACCCATTTAGTACAGGATTTGGCTTCGTCATCCTCTGACTGGA 1608
Db 183 ValSerPheTrpLysThrProValGluCysGlyIleGlyPheThrIleIleLeuSerGly 202
QY 1609 GTCCTCGCTATTATCTCTTTTATTATATATGGGACAAGAACCCAGGTGGTTTAGAATAATG 1668
Db 203 LeuProValTyrPhePheGlyValTrpTrpLysAsnLysProLysTrpLeuGlnGly 222
QY 1669 TCAGAGAAAATAACAGAACATTACAAATAATACTGGAAGTTGTACAGAGAA 1722
Db 223 IlePheSerThrThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 240

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RESULT 9

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US-09-107-532A-5743

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; Sequence 5743, Application US/09107532A
; Patent No. 6583275

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GENERAL INFORMATION:

```

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

```

/ NUMBER OF SEQUENCES: 7310
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: GENOME THERAPEUTICS CORPORATION
/ STREET: 100 Beaver Street
/ City: Waltham
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02354
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD-ROM ISO9660
/ COMPUTER: PC
/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: 60/085,598
/ FILING DATE: 14 May 1998
/ APPLICATION NUMBER: 60/051571
/ FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ariniello, Pamela Deneke
/ REGISTRATION NUMBER: 40,489
/ REFERENCE/DOCKET NUMBER: GTC-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781)893-5007
/ TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 5743:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 525 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Enterococcus faecium
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...525
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5743:
/ US-09-107-532A-5743

Alignment Scores:
Pred. No.: 1.33e-47 Length: 525
Score: 537.50 Matches: 133
Percent Similarity: 48.58% Conservative: 106
Best Local Similarity: 27.03% Mismatches: 224
Query Match: 13.05% Indels: 29
DB: 4 Gaps: 8

US-09-667-170A-440 (1-2239) x US-09-107-532A-5743 (1-525)

QY 214 GGTACCTGCAGGGAATGTTAAACGGGAGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCT 273
Db |||||::: ||| ::::: ||| |||||::: |||
39 GlyTyrVal---GlyLysThrGluArgLysIleGlyArgAspGlyIleLysGlnGluPro 57
QY 274 GGGCAGGACGCCTTT-----TCAGGAAGA 297
Db ::::| | | | |
58 HisProLysSerPheLeuTyrPheTrpAspTrpLeuTrpTyrGluArgGlyGlnGlyMet 77
QY 298 GACGCCTTTTCAGGAAGACAGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAA 357
Db ::::| | | | |
78 GluGluTyrGlnAlaThrProValLysGluValLysIleGluAsnGluLeuLysArgThr 97
QY 358 GTCACCTTTACTAGGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTC 417
Db ::::| | | | |
98 MetGlyPhePheThrAlaLeuSerThrValMetGlyThrValIleGlyAlaGlyValPhe 117
QY 418 ATCTCTCCTAAGGGCGTGTCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGG 477
Db |||||::: ||| |||||::: |||
118 PheLysAlaAlaSerValAlaGluValThrGlySerAlaSerLeuHisMetPheSerTrp 137

QY 478 ACGGTGTGTGGGTCTCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTGGGAACAAC 537
Db ::::| | | | |
138 PheLeuGlyGlyMetIleSerValCysAlaGlyLeuThrGlyAlaGluLeuAlaAla 157
QY 538 ATAAAGAAATCTGGAGGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCT 597
Db ::::| | | | |
158 IleProGluThrGlyGlyMetIleLysTyrIleGluArgIleTyrGlyAsnThrAlaAla 177
QY 598 TTTGTACGAGTCTGGGTGGAACCTCTCATATAATACGCCCTGCAGCTACTGTGTGATATCC 657
Db |||||::: ||| ::::: ||| |||||::: |||
178 PheLeuLeuGlyTrpAlaGlnValValIleTyrPheProAlaAsnValAlaAlaLeuSer 197
QY 658 CTGGCATTGTGACGCTACATTCTGGAACCAATTTTATTCAATGTGAATCCCTGAACTT 717
Db ::::| | | | |
198 IleIlePheGlyThrGlnPheValAsnLeuPhe-----GlyLeu 210
QY 718 GCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA-----GTGATGGTCTTAAAT 768
Db ::::| | | | |
211 SerGlnSerMetIleValProValAlaValThrAlaAlaValSerIleLeuLeuIleAsn 230
QY 769 AGCATGAGTGTCAAGTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGCAGCTCACA 828
Db ::::| | | | |
231 PheLeuGlySerLysAlaGlyGlyAlaPheGlnSerIleThrLeuValCysLysLeuIle 250
QY 829 GCAATTCTGATAATTATAGTCCCTGGAGTTATGCCAGCTAATTAAAGTCAAACGAGAAC 888
Db ::::| | | | |
251 ProLeuPheValIleValIlePheGlyLeuPheArgGlnGluGlyValAspPheGlnLeu 270
QY 889 TTTAAAGACGCTTTTCAGGAAGAGATTCAAGTATTACGGGTTGCCACTGGCTTTTAT 948
Db |||||::: ||| ::::: ||| |||||::: |||
271 PheProIleGlnAlaGlyGluAsnLeuSerPhePheSerAlaLeuGlyAlaGlyLeuLeu 290
QY 949 TATGGAATGTATGATATGCTGGTGGTGTCTTACCTCAACTTTGTTACTGAAGAAGTAGAA 1008
Db |||||::: ||| |||||::: ||| ::::: ||| |||||::: |||
291 AlaThrMetPheAlaTyrAspGlyTyrIleHisValGlyAsnIleSerGlyGluLeuLys 310
QY 1009 AACCCCTGAAAAAACCATTCCTTGTCAATATATATATCCATGGCCATTGTCCACCATGGC 1068
Db |||||::: ||| |||||::: ||| ::::: ||| |||||::: |||
311 LysProAlaLysAspLeuProLysAlaIleSerLeuGlyIleIleGlyIleMetIleVal 330
QY 1069 TATGTGCTGACAAATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTGCTTCA 1128
Db |||||::: ||| |||||::: ||| ::::: ||| |||||::: |||
331 TyrLeuLeuValAsnAlaValPheLeuArgThrAlaSerIleAspGlyValAlaGlyAsn 350
QY 1129 AATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC---TCATTAGCAGTT 1185
Db ::::| | | | |
351 SerAsnAlaAlaSerAspValAlaLysMetIlePheGlyGlyPheGlyArgLeuVal 370
QY 1186 CCGATCTTTGTGCCCTCTCCTGCTTTGGTCCCATGAACGGTGGTGTGTGTGTCTCTCC 1245
Db ::::| | | | |
371 ThrValGlyIleLeuIleSerValTyrGlyThrIleAsnGlyTyrThrLeuThrGlyMet 390
QY 1246 AGTTATTCTATGTTGCGTCTCGAGAGGCTCACCTTCCA-----GAAATCCTCTCCATG 1299
Db |||||::: ||| ::::: ||| |||||::: |||
391 ArgLeuProTyrValMetAlaLysGluAsnLeuProPheSerLysLeuPheAlaLys 410
QY 1300 ATTCATGTCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGCAACCTTTGACAATG 1359
Db ::::| | | | |
411 LeuHisAspLysThrLysValProValAlaAlaGlyIleLeuGluLeuValIleAlaIle 430
QY 1360 ATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTTCCCTCAGTTTGGCAGGTGG 1419
Db |||||::: ||| |||||::: ||| ::::: ||| |||||::: |||
431 GlyMetMetMetIleGlyGlyPheAspThrLeuThrAspMetLeuIlePheValIleTrp 450
QY 1420 CTTTTTATGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCAGATATG 1479
Db ::::| | | | |
451 IlePheTyrThrMetValPheValGlyValIleLeuLeuArgLysLysGluProAspLeu 470
QY 1480 CATCGTCTCTTCAAGGTGCCACTG-----TTCATCCGAGCTTTTCTTCACATGC 1533
Db |||||::: ||| |||||::: ||| ::::: ||| |||||::: |||
471 PheArgProTyrLysValProMetTyrPropheIleProLeuValAlaIleIleGlyGly 490
QY 1534 CTCCTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCCATTTTAGTACAGGATTGGCTTCGTC 1593

TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4001:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...417
SEQUENCE DESCRIPTION: SEQ ID NO: 4001:
US-09-107-532A-4001

Alignment Scores:

Pred. No.:	3,94e-41	Length:	417
Score:	475.50	Matches:	120
Percent Similarity:	50.76%	Conservative:	80
Best local Similarity:	30.46%	Mismatches:	185
Query Match:	11.54%	Indels:	9
DB:	4	Gaps:	6

US-09-667-170A-440 (1-2239) x US-09-107-532A-4001 (1-417)

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QY 337 AAAGTGCAGCTGAAGAGGAAAGTCACTTACTGAGGGAGTCTCCATTATCATTTGGCACC 396
Db 15 LysGlyLysLeuLysArgGluLeuAsnLeuPheGlyAlaLeuAlaThrValMetGlyThr 34
QY 397 ATCAATTGGAGCAGGAATCTTCTATCTCTCTAAGGGCGTGTCCAGAACACGGCGCTG 456
Db 35 ValIleGlyAlaGlyValPhePheLysThrAlaAlaValThrAlaSerThrGlnSerThr 54
QY 457 GGCATGTCTCTGACCATCTGGACGGTGTGGGTCTCTGCTCACTATTGGAGCTTTCT 516
Db 55 SerLeuThrLeuLeuAlaThrLeuLeuGlyGlyPheLeuThrIleCysAlaGlyLeuThr 74
QY 517 TATGCTGAATGGGAACAACATAAAGAAATCTGGAGGTCAATACACATATATTTGGAA 576
Db 75 ValAlaGluLeuAlaThrAlaIleProGluThrGlyGlyAlaValIleGlyAla 94
QY 577 GTCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACCTCTCATATACGCCCT 636
Db 95 AlaTyrGlyLysLeuProSerPheLeuLeuGlyTrpAlaGlnSerLeuIleTyrPhePro 114
QY 637 GCAGCTACTGTGTGATATCCCTGGCATTTGGACGCTACATCTGGAACCATTTTATT 696
Db 115 AlaAsnIleAlaAlaLeuSerIleIlePheAlaThrGlnLeuThrAsnLeuGlnLeu 134
QY 697 CAATGTGAATCCCTGAACCTTGGATCAAGCTCATTACAGCTGGGCATAACTGTAGTG 756
Db 135 SerThrAspTyr---LeuLeuLeuIleAlaValIleThrAlaValSerValThr----- 151
QY 757 ATGTCCTAAATAGCATGAGTGTCAAGTGGAGCGCCCGGATCCAGATTTCTTAACCTTT 816
Db 152 ---GlyLeuAsnLeuLeuGlyThrLysValGlyAlaSerValGlnSerValThrLeuIle 170
QY 817 TGCAAGCTCACAGCAATCTGTATAATTATGATCCCTGGAGTTATGAGCTAATAAAGGT 876
Db 171 ValLysLeuIleProIleAlaValIleIleTrpGlyLeuLeuThrProGlyGlnGly 190
QY 877 CAAACGCAGAACTTTAAAGACGCCCTTTTCAAGGAAGAGAT---TCAAGTATTACGGGTTG 933
Db 191 ThrValGlnLeuPhe---ProIleGluAlaGlyLysAspValThrPheValGluGlyLeu 209
QY 934 CCACTGGCTTTTATATGAATGTATGATATGCTGGCTGGTTTACCTCAACTTTGTT 993
Db 210 SerSerAlaLeuAlaThrLeuPheAlaTyrAspGlyTrpLeuGlyValGlyAlaMet 229
QY 994 ACTGAAGAAGTAGAAACCCCTGAAAAACCATTCCTTGGCAATATGTATATCCATGGCC 1053
Db 1053
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Db 230 AlaArgGluMetLysArgProGluLysAspLeuProLysAlaIleLeuGlyLeuSer 249
QY 1054 ATTGTACCAATTGGCTATGTGTGACAAAATGTGGCTACTTTACGACCAATTAATGCTGAG 1113
Db 250 PheValThrValValTyrLeuLeuIleAsnPheValPheLeuLysThrLeuProIleAsp 269
QY 1114 GAGCTGCTGCTTTCAAANGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1173
Db 270 HisLeuAlaGlyAsnLeuAsnAlaAlaSerGluAlaSerAspValIlePheGlyGlyIle 289
QY 1174 ---TCATTAGCAGTTCCGATCTTTGTTGCCCTCTCTCTGCTTTGGCTCCATGAACGGTGT 1230
Db 290 GlyGlyLysLeuValThrIleGlyIleLeuIleSerValTyrGlyAlaLeuAsnGlyTyr 309
QY 1231 GTGTTTGTCTCTCCAGGTTATTCTATGTTGCTCTCGAGAGGGTCACCTTCCAGAAATC 1290
Db 310 ThrLeuThrGlyIleArgValProTyrAlaMetAlaLeuGluAspLeuProPheSer 329
QY 1291 CTCTCCATGATTATGTCGCGCAGCACACATCTCTTACCAGCTGTTATTGTTTGCACCT 1350
Db 330 LysGlnLeuThrAsnLeuSerLysLysPheThrValProTyrValProAlaValPheGln 349
QY 1351 TTGACAAATG-----ATAATGCTCTTCTCTGAGACCTCGACAGTCTTTTGAATTTCTC 1404
Db 350 LeuAlaValAlaCysIleMetMetSerLeuGlySerPheAspPheLeuThrHisMetLeu 369
QY 1405 AGTTTGGCCAGGTGGCTTTTATTTGGCTGGCAGTTGCTGGGCTGATTATCTTCGATAC 1464
Db 370 IlePheValMetTrpLeuPheThrLeuLeuIleCysIleGlyValSerIleLeuThrLys 389
QY 1465 AAATGCCAGATATGATCGTCTCTTCAAGGTGCCACTGTTTC 1506
Db 390 LysAlaProGluLeuProArgProTyrGlnValProLeuTyr 403
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RESULT 12

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US-08-132-990A-8
; Sequence 8, Application US/08132990A
; Patent No. 5834589
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; APPLICANT: YOSHIMOTO, TAKAYUKI
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,990A
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/084,729
; FILING DATE: 29-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05569
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/899,075
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/806,178
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/627,950
; FILING DATE: 14-DEC-1990
```

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 8105-004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-8864
 TELEX: 66441 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 629 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-132-990A-8

Alignment Scores:

Pred. No.:	4.24e-21	Length:	629
Score:	286.00	Matches:	103
Percent Similarity:	43.16%	Conservative:	80
Best Local Similarity:	24.29%	Mismatches:	183
Query Match:	6.94%	Indels:	58
DB:	2	Gaps:	12

US-09-667-170A-440 (1-2239) x US-08-132-990A-8 (1-629)

```

QY 331 AGAGAGAAAGTGCAGCTGAAGAGAGAAAGTCACTTTACTGAGGGAGTCTCCATTATCAT 390
Db 23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
QY 391 GGCACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGCTCCAGAACACGGGC 450
Db 43 GlySerThrLeuGlyAlaGlyValTyrValLeuAlaGlyAlaValAlaArgGlu----- 60
QY 451 AGCGTGGGCATGTCTCTGACCATC---TGGACGGTGTGTGGGTCTCTGTCACATTATTGGA 507
Db 61 AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaAlaLeuAlaSerValLeuAla 80
QY 508 GCTTTGTCTTATGCTGAATGGGAACAACATAAAGAAATCTGGAGGTCAATACATAT 567
Db 81 GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
QY 568 ATTTTGAAGCTTTTGGTCCATTACCATCTTTTGTACGAGTCTGGGTGGAACTCTC--- 624
Db 101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
QY 625 ---ATAATACGCCCTGCAGCTACTGCT---GTGATATCCCTGGCATTGGACGCTACATT 678
Db 121 TyrIleIleGlyThrSerSerValAlaAlaArgAlaTrpSerAlaThrPheAspGluLeuIle 140
QY 679 CTGGAACCATTT-----TTTATTCAA 699
Db 141 GlyArgProIleGlyGluPheSerArgThrHisMetThrLeuAsnAlaProGlyValLeu 160
QY 700 TGTGAAATCCCTGAACCTTGGCATCAAGCTCATTACAGCTGTGGGCATACTAGTAGTATG 759
Db 161 AlaGluAsnProAspIlePheAlaValIleIle-----IleLeuIleLeuThr 176
QY 760 GTCCTAAATAGCATGAGTGTACAGCTGGAGCGCCCGGATCCAGATTTTCTTAACCTTTTGC 819
Db 177 GlyLeuLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle 196
QY 820 AAGCTCAGCAATCTTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAA 879
Db 197 AsnValLeuValLeuGlyPheIleMetValSerGly-----PheValLysGlySer 213
QY 880 ACGCAGAACTTTAA----- 894
Db 214 ValLysAsnTrpGlnLeuThrGluGluAspPheGlyAsnThrSerGlyArgLeuCysLeu 233
QY 895 -----GACGCTTTTTCAGGAAGAGATTCAAGTATTACGGGTGGCTGCTGCTTTTAT 948
Db 234 AsnAsnAspThrLysGluGlyLysProGlyValGlyGlyPheMetPropGlyPheSer 253

```

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QY 949 TATGGAATG-----TATGCATATGCTGGCTGGTTTACCTCAAC 987
Db 254 GlyValLeuSerGlyAlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAla 273
QY 988 TTTGTTACTGAAGAAGTAGAAAAACCTGAAAAAACCAATTCCCTTGAATATGTATATCC 1047
Db 274 ThrThrGlyGluGluValLysAsnProGlnLysAlaIleProValGlyIleValAlaSer 293
QY 1048 ATGGCCATTGTACCATTTGGCTATGTGCTGACAAATGGCTACTTTACGACCATTAAT 1107
Db 294 LeuLeuIleCysPheIleAlaTyrPhe-----GlyValSerAlaAlaLeuThrLeuMet 311
QY 1108 GCTGAGGAGCTGCTTTTCAAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGA 1167
Db 312 MetProTyrPheCysLeuAspAsnAsnSerProLeuProAspAlaPheLysHisValGly 331
QY 1168 -----AATTTCTCATTAGCAGTTCCGATCTTTTGTGGCCTCTCTGCTTTGGC 1215
Db 332 TrpGluGlyAlaLysTyrAlaValAlaValGlySerLeuCysAlaLeuSer-----Ala 349
QY 1216 TCCATGAACGGTGTGTGTTTGTCTCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGGT 1275
Db 350 SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAspGly 369
QY 1276 CACCTTCCAGAAATCTCTCCATGATTTCATGTCGCAAGCACACTCTACCATGCTTT 1335
Db 370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProIleAlaThr 389
QY 1336 ATTGTTTTCACCTTTGACAAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTG 1395
Db 390 LeuAlaSerGlyAlaValAlaAlaValMetAlaPheLeuPheAspLeuLysAspLeuVal 409
QY 1396 AATTTCTCAGTTTGGCAGGTGGCTTTTATGGGCTGGCAGTTGCTGGGCTGATTTAT 1455
Db 410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
QY 1456 CTTGCATACAAA 1467
Db 430 LeuArgTyrGln 433

```

RESULT 13

PCT-US92-09382-8

; Sequence 8, Application PC/TUS9209382

; GENERAL INFORMATION:

; APPLICANT: MERUELO, DANIEL

; APPLICANT: YOSHIMOTO, TAKAYUKI

; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding

; TITLE OF INVENTION: Therefor

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.24

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/09382

; FILING DATE: 19921213

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Livnat, Shmuel

; REGISTRATION NUMBER: 33,949

; REFERENCE/DOCKET NUMBER: MERUELO=1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 628-5197

; INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-09382-8

Alignment Scores:
Pred. No.: 4.24e-21 Length: 629
Score: 286.00 Matches: 103
Percent Similarity: 43.16% Conservative: 80
Best Local Similarity: 24.29% Mismatches: 183
Query Match: 6.94% Indels: 58
DB: 5 Gaps: 12

US-09-667-170A-440 (1-2239) x PCT-US92-09382-8 (1-629)

QY 331 AGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCAT 390
| | | | | : : : : : | | | : : : : :
Db 23 ArgGluGluThrArgLeuSerArgCysLeuAsnThrPheAspLeuValAlaLeuGlyVal 42
QY 391 GGCACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGTCTCCAGAACACGGGC 450
| | | : : : | | | | | : : : : : | | | : : :
Db 43 GlySerThrLeuGlyAlaGlyValThrValLeuAlaGlyAlaValAlaArgGlu----- 60
QY 451 AGCGTGGGCATGTCTCTGACCATC---TGGACGGTGTGTGGGTCCTGTCTACTATTGGA 507
: : : | | | : : : : : | | | : : : : : | | | : : :
Db 61 AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaAlaLeuAlaSerValLeuAla 80
QY 508 GCTTTGTCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATAT 567
| | | | | | | | | | | | | | | : : : | | | | |
Db 81 GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr 100
QY 568 ATTTTGGAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTC--- 624
| | | | | | | | | | | | | | | : : : | | | | |
Db 101 SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer 120
QY 625 ---ATAATACCCCTGCAGCTACTGCT---GTGATATCCCTGGCATTGGACGCTACATT 678
| | | | | : : : : : | | | | | | | | | | |
Db 121 TyrIleIleGlyThrSerSerValAlaArgAlaTrpSerAlaThrPheAspGluLeuIle 140
QY 679 CTGGAACCATTT-----TTTATTCAA 699
| | | : : :
Db 141 GlyArgProIleGlyGluPheSerArgThrHisMetThrLeuAsnAlaProGlyValLeu 160
QY 700 TGTGAAATCCCTGAACTTGCAGATCAAGCTCATTACAGCTGTGGGCATACTGTAGTGANG 759
| | | | | : : : : : | | | | | | | | | | |
Db 161 AlaGluAsnProAspIlePheAlaValIleIle-----IleLeuIleLeuThr 176
QY 760 GTCCTAAATAGCATGAGTGTGAGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGC 819
| | | : : : : : | | | | | : : : | | | | |
Db 177 GlyLeuLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle 196
QY 820 AAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAA 879
: : : : : | | | : : : : : | | | : : : : :
Db 197 AsnValLeuValLeuGlyPheIleMetValSerGly-----PheValLysGlySer 213
QY 880 ACGCAGAACTTTAA-----894
: : : | | | : : : : :
Db 214 ValLysAsnTrpGlnLeuThrGluGluAspPheGlyAsnThrSerGlyArgLeuCysLeu 233
QY 895 -----GACGCCTTTTTCAGGAAGAGATTCAAGTATTACGGGTTGCCACTGGCTTTTAT 948
| | | | | : : : : : | | | : : : : :
Db 234 AsnAsnAspThrLysGluGlyLysProGlyValGlyPheMetProPheGlyPheSer 253
QY 949 TATGGAATG-----TATGATATGCTGGCTGGTTTACCTCAAC 987
: : : | | | : : : : : | | | : : : : :
Db 254 GlyValLeuSerGlyAlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAla 273
QY 988 TTTGTTACTGAAGAGTAGAAACCCCTGAAAAACCATTCCTTCCCTTGGCAATATGATATCC 1047
| | | | | : : : : : | | | | | : : : : :
Db 274 ThrThrGlyGluGluValLysAsnProGlnLysAlaIleProValGlyIleValAlaSer 293

QY 1048 ATGGCCATTGTACACATTGGCTATGTGCTGACAAAATGTGGCCTACTTTTACACCATTAAT 1107
: : : | | | | | | | | | : : : : :
Db 294 LeuLeuIleCysPheIleAlaTyrPhe-----GlyValSerAlaAlaLeuThrLeuMet 311
QY 1108 GCTGAGGAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGTACTGGGA 1167
| | | | | | | | | : : : : : | | | : : : : :
Db 312 MetProTyrPheCysLeuAspAsnSerProLeuProAspAlaPheLysHisValGly 331
QY 1168 -----AATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCTCTGCTTTGGC 1215
: : : : : : : : | | | | | | | | | | |
Db 332 TrpGluGlyAlaLysTyrAlaValAlaValGlySerLeuCysAlaLeuSer-----Ala 349
QY 1216 TCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGT 1275
| | | : : : | | | : : : | | | : : : | | | : : :
Db 350 SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAspGly 369
QY 1276 CACCTTCCAGAAATCCTCTCCATGATTCTCCGCAAGCACACTCTCTACCACTGTT 1335
| | | : : : | | | : : : | | | : : : | | | : : :
Db 370 LeuLeuPheLysPheLeuAlaAsnValAsnAspArgThrLysThrProIleIleAlaThr 389
QY 1336 ATTGTTTTCACCCCTTGCACAAATGATAATGCTCTTCTGAGACCTCGACAGTCTTTTG 1395
: : : : : : : : | | | | | | | | | | |
Db 390 LeuAlaSerGlyAlaValAlaAlaValMetAlaPheLeuPheAspLeuLysAspLeuVal 409
QY 1396 AATTTCTCAGTTTGGCAGGTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTAT 1455
: : : : : | | | | | | | | | : : : : :
Db 410 AspLeuMetSerIleGlyThrLeuLeuAlaTyrSerLeuValAlaAlaCysValLeuVal 429
QY 1456 CTTTCGATACAAA 1467
| | | | | : : :
Db 430 LeuArgTyrGln 433

RESULT 14.

US-09-134-001C-4290
; Sequence 4290, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4290

; LENGTH: 521

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4290

Alignment Scores:

Pred. No.: 8.97e-21 Length: 521
Score: 282.50 Matches: 135
Percent Similarity: 43.39% Conservative: 108
Best Local Similarity: 24.11% Mismatches: 206
Query Match: 6.86% Indels: 111
DB: 4 Gaps: 26

US-09-667-170A-440 (1-2239) x US-09-134-001C-4290 (1-521)

QY 127 TTTTAT---CATATTCTGGATTTTGTGGATCTTTTGTGTTTCTCATCATCTGGATTCAGGA 183
| | | | | : : : | | | | | | | | | | |
Db 8 PheTyrLeuHisValAspPheLeuIleArgIleValLysGluCysLeuLeuThr-- 26
QY 184 AAGCCTGTTGTCTCCACCATCTCCAAAGGAGGTTACCTGCAGGGAAATGTTAACGGGAGG 243
| | | | | : : : : : | | | : : : : :
Db 27 ---HisValAsnSerLysLeuMetLeuTrpArgPheValMetGlySerPheAsnArg 45
QY 244 CTGCTTCCCTGGGCAACAAGGAGGCCACCTGGGCGAGGACGCTTTTTCAGGAAGAGACGCC 303

Db 46 MetThr-----ArgLysGluAsnPro-----ThrIle 54
QY 304 TTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCGAGTGAAGAGGAAAGTCACT 363
Db 55 TyrGlnSerLysAspGly-----HisLeuLysArgThrLeuArg 67
QY 364 TTAAGGAGGAGTCTCCATTATCAATGGCACCACATCATTTGGAGCAGGAATCTTCACTCT 423
Db 68 ValArgAspPheLeuAlaLeuGlyValGlyThrIleValSerThrSerIlePheThrLeu 87
QY 424 CCTAAGGGCGTGCTCCAGAACACACGGCGAGCGTGGGCATGTCTCTGACCATCTGGACGGTG 483
Db 88 ProGlyValValAlaAlaAlaGluHisAlaGlyProAlaValSerLeuSer--PheLeuLeu 106
QY 484 TGTGGGTCCTGTCACATATTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACATAAAG 543
Db 107 AlaAlaIleValAlaGlyLeuValAlaPheThrTyrAlaGluMetAlaSerThrMetPro 126
QY 544 AAATCTGGAGTCAATACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTGTGA 603
Db 127 PheAlaGlySerAlaTyrSerTrpIleAsnValLeuPheGlyGluLeuPheGlyTrpVal 146
QY 604 CGAGTCTGGTGAACCTCCTCATATAATACCCCTGCAGCTACTGCTGTGATATCCCTGGCA 663
Db 147 AlaGlyTrpAla--LeuLeuAlaGluTyrPheIleAlaValAlaPheValAlaSerGly 165
QY 664 TTTTGA-----CGCTACATTTCTGGAACCATTTTATTCAATGTGAATCCCTGAA 714
Db 166 PheSerAlaAsnLeuArgGlyLeuIleAlaProLeuGlyIle-----SerLeuProLys 183
QY 715 CTT-----GCGATCAAGCTCAATACAGCTGTGGGC 744
Db 184 SerLeuSerAsnProPheGlySerAsnGlyGlyValIleAspIleIleAlaAlaVal 203
QY 745 ATAAGTGTAGTGGTCTCTAAATAGCATGAGTGTGAGCTGGAGCGCCGGATCCAGATT 804
Db 204 IleIleLeuThrAlaLeuLeuLeuSerArgGlyMetAsnGluAlaAlaArgMetGluAsn 223
QY 805 TTCTTAACCTTTTGAAGCTCACAGCAATTCGATAATTATAGTCCCTGGAGTTATGCAG 864
Db 224 ValLeuValIleLeuLysValLeuAlaIleIleLeuPheValIleValGlyLeuThrAla 243
QY 865 CTAATTAAAGGTCAAACGACAACTTTAAAGAC----- 897
Db 244 Ile-----AsnPheSerAsnTyrIleProPheIleProGluHisLys 257
QY 898 -----GCCTTTTCAGGAAGAGATCAAGTATTACGGCGTGTGCCACTGGCT 942
Db 258 ValThrGluThrGlyAspPheGlyGly----- 266
QY 943 TTTTATTATGAATGTATGCATATGCTGGTGGTGTACCTCAACTTTGTT----- 993
Db 267 ---TrpGlnGlyIleTyrAlaGlyValSerMetIlePheLeuAlaTyrIleGlyPheAsp 285
QY 994 -----ACTGAAGAAGTAGAARACCCCTGAAAAAACCAATCCCTTGCAATA 1038
Db 286 SerIleAlaAlaAsnSerAlaGluAlaIleAsnProGlnLysThrMetProArgGlyIle 305
QY 1039 TGTATATCCATGGCCATT-----GTCACCATTGGCTATGCTGACAAAT 1083
Db 306 LeuGlySerLeuIleValAlaIleValLeuPheValAlaValAlaLeuValLeuValGly 325
QY 1084 GTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTGCTTTCAAAATGAGTGGCAGTG 1143
Db 326 MetPheHisTyrSerGln-----TyrAlaAspAsnAlaGluProVal 339
QY 1144 ACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCA-----GTTCCGATCTTTGTT 1197
Db 340 GlyTrpAlaLeuArgGluSerGlyHisGlyIleIleAlaAlaIleValGlnAlaIleSer 359
QY 1198 GCCCTCTCTGCTTTGGTCCCATGAACGGTGGTGGTGTGCTGTCTCCAGTTATTCTAT 1257

Db 360 ValIleGlyMetPheThrAlaLeuIleGlyMetMetLeuAlaGlySerArgLeuLeuTyr 379
QY 1258 GTTGGCTCTCGAGAGGTCACTTCCAGAAATCCTCTCCATGATTCAATGTCGCGAAGCAC 1317
Db 380 SerPheGlyArgAspGlyLeuLeuProSerTrpLeuSerGlnLeuAsn--HisLysHis 398
QY 1318 ACTCCTCTACCAGCTGTATTGTTTTCACCCCTTTGACAAATGATAATGCTCTCTCTGGA 1377
Db 399 LeuProAsnArgAlaLeuAlaIle-----LeuThrIleIleGlyValValIleGly 415
QY 1378 GAC-----CTCGACAGTCTTTTGAATTTCTCAGTTTTCAGTTTTCAGGTGG 1419
Db 416 SerMetPheProPheAlaPheLeuAlaGlnLeuIleSerAlaGlyThrLeuValAlaPhe 435
QY 1420 CTTTATTGGGCTGGCAGTTGCTGGGCTGATTATCTTCGATACAAATGCCACATATG 1479
Db 436 MetPheValSerLeuAlaMetTyrArgLeu-----ArgLysArgGluGlyLysAspLeu 453
QY 1480 CATCGTCTCT--TTCAAGGTGCCACTGTTTC-----ATCCCAGCTTTGTTTCTTCACA 1530
Db 454 ProLysProGluPheLysLeuProLeuTyrProIleLeuProAlaIle--ThrPheIle 472
QY 1531 TGCCTCTTCATGGTTGCCCTTTCCCTC---TATTGGACCCCATTTAGTACAGGATTGGC 1587
Db 473 LeuValLeuLeuValPheTrpGlyLeuSerPheGluAlaLysLeuTyrThrLeuIleTrp 492
QY 1588 TTCGTCACTCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGGGACAAGAAA 1647
Db 493 PheIleVal-----GlyIleIleIleTyrLeuIleTyrGlyIleArgHisSerLys 509
RESULT 15
US-08-132-990A-4
; Sequence 4, Application US/08132990A
; Patent No. 5834589
; GENERAL INFORMATION:
; APPLICANT: MERUELO, DANIEL
; APPLICANT: YOSHIMOTO, TAKAYUKI
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,990A
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/084,729
; FILING DATE: 29-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05569
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/899,075
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/806,178
; FILING DATE: 13-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/627,950
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8105-004-999

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66441 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-132-990A-4

Alignment Scores: 2.03e-20 Length: 622
Pred. No.: 279.50 Matches: 102
Score: 42.82% Conservative: 80
Percent Similarity: 24.00% Mismatches: 176
Best Local Similarity: 6.78% Indels: 67
Query Match: 2 Gaps: 13
DB:

US-09-667-170A-440 (1-2239) x US-08-132-990A-4 (1-622)

QY	331	AGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACCTTTACTGAGGGAGTCTCCATTATCATT	390
Db	23	ArgGluGluSerArgLeuSerArgCysLeuAsnThrTyrAspLeuValAlaLeuGlyVal	42
QY	391	GGACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGTCTCCAGAACACGGGC	450
Db	43	GlySerThrLeuGlyAlaGlyValTyrValLeuAlaGlyAlaValAlaArgGlu-----	60
QY	451	AGCGTGGCATGTCTCTGACCATC---TGGACGGTGTGTGGGGTCTCTCACTATTGGA	507
Db	61	AsnAlaGlyProAlaIleValIleSerPheLeuIleAlaAlaLeuAlaSerValLeuAla	80
QY	508	GCTTTGTCTATGTCTGAATTGGGAACACTATAAGAAATCTGGAGTCAATTACACATAT	567
Db	81	GlyLeuCysTyrGlyGluPheGlyAlaArgValProLysThrGlySerAlaTyrLeuTyr	100
QY	568	ATTTTGGAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTC---	624
Db	101	SerTyrValThrValGlyGluLeuTrpAlaPheIleThrGlyTrpAsnLeuIleLeuSer	120
QY	625	---ATAATACGCCCTGCAGCTACTGTCT---GTGATATCCCTGGCATTGGACGCTACATT	678
Db	121	TyrIleIleGlyThrSerSerValAlaArgAlaTrpSerAlaThrPheAspGluLeuIle	140
QY	679	CTGGAACCATTT-----TTTATTCAA	699
Db	141	GlyLysProIleGlyGluPheSerArgGlnHisMetAlaLeuAsnAlaProGlyValLeu	160
QY	700	TGTGAATCCCTGAACCTTGCAGTCAAGCTCATTACAGCTGTGGGCATAACTGTAGTGATG	759
Db	161	AlaGlnThrProAspIlePheAlaValIleIle-----IleIleIleLeuThr	176
QY	760	GTCCTAAATAGCATGTGTCAAGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGC	819
Db	177	GlyLeuLeuThrLeuGlyValLysGluSerAlaMetValAsnLysIlePheThrCysIle	196
QY	820	AAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAAGGTCAA	879
Db	197	AsnValLeuValLeuCysPheIleValValSerGly-----PheValLysGlySer	213
QY	880	ACGCAGAACTTTAAAGACGCCCTTTTTCAGGAAGAGATTCAAGTATTACGGGTTGCCACTG	939
Db	214	IleLysAsnTrpGln-----LeuThrGluLysAsnPheSerCysAsnAsnAspThr	231
QY	940	GCTTTTATTATGGA-----	954
Db	232	AsnValLysTyrGlyGluGlyGlyPheMetProPheGlyPheSerGlyValLeuSerGly	251
QY	955	-----ATGATGCATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAA	1002

Db	252	AlaAlaThrCysPheTyrAlaPheValGlyPheAspCysIleAlaThrThrGlyGluGlu	271
QY	1003	GTAGAAAACCCCTGAAAAAACCACTTCCCTTGCATAATGTATATCCATGGCCATTGTCAAC	1062
Db	272	VallysAsnProGlnLysAlaIleProValGlyIleValAlaSerLeuLeuIleCysPhe	291
QY	1063	ATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTG	1122
Db	292	Ile-----AlaTyrPhe---GlyValSerAlaAlaLeuThrLeu	303
QY	1123	CTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC-----	1173
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QY	1174	-----TCATTAGCAGTTCCGATCTTTGTTGCCCTCTCTCTGCTTT	1212
Db	324	GlyTrpGluGluAlalysTyrAlaValAlaIleGlySerLeuCysAlaLeuSerThr---	342
QY	1213	GGCTCCATGAACGGTGTGTGTTTGTCTGTCTCCAGGTTATCTATGTTGGTCTCGAGAG	1272
Db	343	---SerLeuLeuGlySerMetPheProMetProArgValIleTyrAlaMetAlaGluAsp	361
QY	1273	GGTCACCTTCCAGAAATCCTCTCCATGATTCAATGTCGCAAGCACACTCCTCTACAGCT	1332
Db	362	GlyLeuLeuPheLysPheLeuAlaLysIleAsnAsnArgThrLysThrProValIleAla	381
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Db	382	ThrValThrSerGlyAlaIleAlaAlaValMetAlaPheLeuPheGluLeuLysAspLeu	401
QY	1393	TTGAATTTCTCAGTTTTGGCAGGTGGCTTTTATTGGCTGGCAGTTGCTGGGCTGATT	1452
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QY	1453	TATCTTCGATACAAA	1467
Db	422	ValLeuArgTyrGln	426

Search completed: October 31, 2003, 11:07:49
Job time : 64.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 31, 2003, 11:02:11 ; Search time 200 Seconds
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3831.960 Million cell updates/sec

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Perfect score: 4120
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Searched: 642050 seqs, 171146064 residues

Total number of hits satisfying chosen parameters: 1284100

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	2519	61.1	501	15	US-10-163-866-48	Sequence 48, Appl
2	2519	61.1	501	15	US-10-163-866-49	Sequence 49, Appl
3	2298	55.8	502	12	US-10-214-867A-13	Sequence 13, Appl
4	1210.5	29.4	507	15	US-10-163-866-54	Sequence 54, Appl
5	1206.5	29.3	524	15	US-10-163-866-37	Sequence 37, Appl
6	1198.5	29.1	507	15	US-10-163-866-38	Sequence 38, Appl
7	1198.5	29.1	507	15	US-10-163-866-39	Sequence 39, Appl
8	1198	29.1	512	12	US-10-214-867A-10	Sequence 10, Appl
9	1156.5	28.1	515	12	US-10-214-867A-12	Sequence 12, Appl
10	1156.5	28.1	515	15	US-10-163-866-40	Sequence 40, Appl
11	1131.5	27.5	511	15	US-10-163-866-41	Sequence 41, Appl
12	1131.5	27.5	511	15	US-10-163-866-42	Sequence 42, Appl
13	1111.5	27.0	511	12	US-10-214-867A-11	Sequence 11, Appl
14	1101.5	26.7	535	15	US-10-163-866-43	Sequence 43, Appl
15	1101.5	26.7	535	15	US-10-163-866-44	Sequence 44, Appl
16	1097	26.6	533	12	US-10-214-867A-9	Sequence 9, Appl
17	1075.5	26.1	487	15	US-10-163-866-46	Sequence 46, Appl
18	1067.5	25.9	487	15	US-10-163-866-45	Sequence 45, Appl
19	1051.5	25.5	530	12	US-10-214-867A-1	Sequence 1, Appl
20	1048	25.4	517	10	US-09-815-923-16	Sequence 16, Appl
21	1039	25.2	523	12	US-10-214-867A-4	Sequence 4, Appl
22	1039	25.2	523	15	US-10-163-866-47	Sequence 47, Appl
23	732	17.8	414	9	US-09-925-297-747	Sequence 747, App
24	513	12.5	97	10	US-09-738-973-586	Sequence 586, App
25	513	12.5	97	10	US-09-854-133-586	Sequence 586, App
26	513	12.5	97	15	US-10-144-649A-586	Sequence 586, App
27	513	12.5	114	15	US-10-144-649A-742	Sequence 742, App
28	412.5	10.0	180	15	US-10-163-866-50	Sequence 50, Appl
29	406.5	9.9	179	9	US-09-864-761-43216	Sequence 43216, A
30	401	9.7	166	12	US-10-029-386-32531	Sequence 32531, A
31	351	8.5	507	15	US-10-156-761-9780	Sequence 9780, Ap
32	327.5	7.9	492	15	US-10-156-761-14414	Sequence 14414, A
33	323	7.8	462	12	US-10-287-274-345	Sequence 345, App
34	322	7.8	456	9	US-09-815-242-4932	Sequence 4932, Ap
35	322	7.8	463	9	US-09-815-242-10662	Sequence 10662, A
36	303.5	7.4	472	15	US-10-156-761-14823	Sequence 14823, A
37	303.5	7.4	480	15	US-10-156-761-9855	Sequence 9855, Ap
38	295	7.2	619	10	US-09-741-153-4	Sequence 4, Appl
39	295	7.2	619	12	US-10-353-958-4	Sequence 2, Appl
40	286.5	7.0	619	10	US-09-741-153-2	Sequence 2, Appl
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42	286	6.9	629	15	US-10-157-031-34	Sequence 34, Appl
43	262	6.4	470	9	US-09-815-242-12078	Sequence 12078, A
44	257.5	6.2	482	9	US-09-815-242-12941	Sequence 12941, A
45	255.5	6.2	489	15	US-10-156-761-8760	Sequence 8760, Ap

ALIGNMENTS

RESULT 1
US-10-163-866-48
; Sequence 48, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 501


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-48

Alignment Scores:
Pred. No.:      2.41e-228      Length:      501
Score:          2519.00        Matches:      498
Percent Similarity: 96.51%      Conservative: 0
Best Local Similarity: 96.51%    Mismatches: 0
Query Match:     61.14%        Indels:      18
DB:              15            Gaps:        1

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QY 244 CTGCCTTCCCTGGGCAACAAGGAGGCCACCTGGGCAGGACGCCCTTTCAGGAAGAGACGCC 303
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Db 24 LeuProSerLeuGlyAsnLysGluProGlyGln----- 35

QY 304 TTTTCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACT 363
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Db 36 -----GluLysValGlnLeuLysArgLysValThr 45

QY 364 TTA CTGAGGGAGTCTCCATTATCATTTGGACCACATCATTTGGAGCAGGAATCTTCATCTCT 423
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QY 424 CCTAAGGGCGTGTCCAGAAACACGGGCGAGCGTGGGCATGTCTCTGACCATCTGGACGGTG 483
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QY 484 TGTGGGTCCTGTCACTATTGTGGAGCTTTGTCTTATGCTGAATTTGGCAACAATAAAG 543
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QY 544 AAATCTGGAGTCATTACACATATATTTTGGAGTCTTTTGGTCCATTACCAGCTTTTGTA 603
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; Sequence 49, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-49
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Score: 2519.00 Matches: 498
Percent Similarity: 96.51% Conservative: 0
Best Local Similarity: 96.51% Mismatches: 0
Query Match: 61.14% Indels: 18
DB: 15 Gaps: 1

US-09-667-170A-440 (1-2239) x US-10-163-866-49 (1-501)

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Db	106	LysSerGlyGlyHisTyrThrTyrIleLeuGluValPheGlyProLeuProAlaPheVal	125
QY	604	CGAGTCTGGGTGGAACCTCCTCATATAATPACGCCCTGCAGCTACTGCTGTGATATCCCTGGCA	663
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QY	724	AAGCTATTACAGCTGTGGGCATAACTGTAGTGTGTCCTTAATAGCATGAGTGTGACG	783
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QY	964	TATGCTGGCTGGTTTTTACCTCAACTTTTGTACTGAAGAAGTAGAAAACCTGAAAAACC	1023
Db	246	TyrAlaGlyTrpPheTyrLeuAsnPheValThrGluGluValGluAsnProGluLysThr	265
QY	1024	ATTCCTCCCTTGCAATATGTATATCCATGGCCATTGTCACCATTGGCTATGTGCTGACAAAT	1083
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QY	1384	GACAGCTCTTTTGAATTTCTCAGTTTGGCCAGTGGCTTTTATTGGGCTGGCAGTTGCT	1443
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Db	426	PheIleProAlaLeuPheSerPheThrCysLeuPheMetValAlaLeuSerLeuTyrSer	445
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US-10-214-867A-13
; Sequence 13, Application US/10214867A
; Publication No. US2003014844A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-214-867A-13

Alignment Scores:
Pred. No.: 1.64e-207 Length: 502
Score: 2298.00 Matches: 443
Percent Similarity: 92.82% Conservative: 35
Best Local Similarity: 86.02% Mismatches: 19
Query Match: 55.78% Indels: 18
DB: 12 Gaps: 1

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QY 547 TCTGGAGGTCAATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTTGTACGA 606
Db 130 SerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAlaPheLeuLys 149
QY 607 GTCGTGGTGGAACCTCCTCATATAATACGCCCTGCAGTACTGTGTGATATCCCTGGCATTT 666
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QY 727 CTCATTACAGCTGTGGGCATACTGTAGTATGTCCTCAATAGCATGAGTGTGAGCTGG 786
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QY 787 AGCGCCGGATCCAGATTTTCTTAACCTTTTGCAAGCTCACAGCAATTTCTGATAATATA 846
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Db 310 AsnLeuAlaTyrPheThrThrLeuSerThrGluGlnMetLeuSerSerGluAlaValAla 329
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Db 510 ThrValLeuCysGlnLysLeuMetGlnValValProGlnGlu 523
RESULT 6
US-10-163-866-38
; Sequence 38, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-38
Alignment Scores:
Pred. No.: 7,25e-104 Length: 507
Score: 1198.50 Matches: 231
Percent Similarity: 65.79% Conservative: 94
Best Local Similarity: 46.76% Mismatches: 166
Query Match: 29.09% Indels: 3
DB: 15 Gaps: 2
US-09-667-170A-440 (1-2239) x US-10-163-866-38 (1-507)
QY 247 CCTTCCCTGGGCAACAAGAGGCCACCTGGGAGGACGCCTTTTTCAGGAAGAGACGCCTTT 306
Db 14 ProValAlaGluGluLysGluGluAlaArgGluLysMetLeuAlaSerLysArgAlaAsp 33
QY 307 TCAGGAAGAGACGCCTTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAGAAAGTCACTTTA 366
Db 34 GlyAlaAlaProAlaGlyGluGly---GluGlyValThrLeuGlnArgAsnIleThrLeu 52
QY 367 CTGAGGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTCTCCT 426
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Db 73 ThrGlyValLeuLysGluAlaGlySerProGlyLeuAlaLeuValMetTrpAlaAlaCys 92
QY 487 GGGGTCCTGCTCACTATTGGAGCTTTTGTCTTATGCTGAATTGGGAACAACATAAAGAAA 546

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QY 727 CTCATTACAGCTGTGGGCATAAAGTGTAGTGATGGTCCCTAAATAGCATGAGTGTGCTGG 786
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QY 1021 ACCATTCCCCTTGCAATATGATATATCCATGGCCATTGTCCATTGGCTATGGTGTGACA 1080
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QY 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCC 1200
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RESULT 7
US-10-163-866-39
; Sequence 39, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-39
Alignment Scores:
Pred. No.: 7.25e-104 Length: 507
Score: 1198.50 Matches: 231
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US-09-667-170A-440 (1-2239) x US-10-163-866-39 (1-507)
QY 247 CCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGACGCCCTTTTCAGGAAGACGCGCTTT 306
Db 14 ProValAlaGluGluLysGluGluAlaArgGluLysMetLeuAlaSerLysArgAlaAsp 33
QY 307 TCAGGAAGAGACGCCCTTTTCAGGAAGAGAGAAAGTCAGCTGAAGAGGAAAGTCACTTTA 366
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QY 487 GGGGTCTGTCACTATTGGAGCTTTTGTCTTATGCTCAATTGGGACAACTATAAAGAAA 546
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QY 907 -----GGAAGAGATTCAAGTATTACCGGGTTGCCACTGGCTTTTATTATGGAATGAT 960
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Db 493 ThrValLeuCysGlnLysIleuMetGlnValValProGlnGlu 506
RESULT 8
US-10-214-867A-10
; Sequence 10, Application US/10214867A
; Publication No. US2003014844A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL, AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-214-867A-10
Alignment Scores:
Pred. No.: 8.12e-104 Length: 512
Score: 1198.00 Matches: 229
Percent Similarity: 67.36% Conservative: 95
Best Local Similarity: 47.61% Mismatches: 151
Query Match: 29.08% Indels: 6
DB: 12 Gaps: 2

US-09-667-170A-440 (1-2239) x US-10-214-867A-10 (1-512)
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QY 358 GTCACCTTTACTGAGGGAGTCTCCATTATCATATTGGCACCATCATTTGGAGCAGGAATCTTC 417
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Db 111 IleSerLysSerGlyGlyAspTyrAlaTyrMetLeuGluValTyrGlySerLeuProAla 130
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QY 658 CTGGCATTTTGGACGCTACATTCTGGAACCACTTTTATTCAATGTGAATCCCTGAACCTT 717
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397 TyrTrpPhePheValGlyLeuSerValValGlyGlnLeuTyrLeuArgTrpLysGluPro 416

QY 1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTCTTCACATGC 1533
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
417 LysArgProArgProLeuLysLeuSerValPhePheProIleValPheCysIleCysSer 436

QY 1534 CTCCTTCATGTTGCCCTTTCCCTCTATTCCGACCCCATTTAGTACAGGATTGGCTTCGTC 1593
Db      ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
437 ValPheLeuValIleValProLeuPheThrAspThrIleAsnSerLeuIleGlyIleGly 456

QY 1594 ATCACTTGACTGGAGTCCCTGGTATTATCTC-----TTTATTATATGGACAAAGAAA 1647
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
457 IleAlaLeuSerGlyValProPheTyrPheMetGlyValTyrLeuProGluSerArgArg 476

QY 1648 CCCAGGTGTTTAGAATAATGTCAGAGAAAATAACCAGAA---ACATTACAAATAATACTG 1704
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
477 ProLeuPheIleArgAsnValLeuAlaAlaIleThrArgGlyThrGlnGlnLeuCysPhe 496

QY 1705 GAAGTTGTACCAAGAAGAAGAT 1725
Db      ||||| ||||| |||||
497 CysValLeuThrGluLeuAsp 503
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RESULT 10

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US-10-163-866-40
; Sequence 40, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 515
```

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-40

Alignment Scores:
Pred. No.: 6.64e-100 Length: 515
Score: 1156.50 Matches: 218
Percent Similarity: 69.16% Conservative: 105
Best Local Similarity: 46.68% Mismatches: 141
Query Match: 28.07% Indels: 3
DB: 15 Gaps: 2

US-09-667-170A-440 (1-2239) x US-10-163-866-40 (1-515)

QY 334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC 393
Db      ||| ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
37 GluThrMetGlnLeuLysLysGluIleSerLeuLeuAsnGlyValSerLeuValValGly 56

QY 394 ACCATCATTTGGAGCAGGAATCTTCACTCTCTCCTAAGGGCGTCTCCAGAACACGGGCAGC 453
Db      ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
57 AsnMetIleGlySerGlyIlePheValSerProLysGlyValLeuValHisThrAlaSer 76

QY 454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCACTATTTGGAGCTTTG 513
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
77 TyrGlyMetSerLeuIleValTrpAlaIleGlyGlyLeuPheSerValValGlyAlaLeu 96

QY 514 TCTTATGCTGAATTGGGAACAACATAAAGAAATCTGGAGGTCACTATATATATTTTG 573
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
97 CysTyrAlaGluLeuGlyThrThrIleThrLysSerGlyAlaSerTyrAlaTyrIleLeu 116

QY 574 GAAGTCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATATAACGC 633
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
117 GluAlaPheGlyGlyPheIleAlaPheIleArgLeuTrpValSerLeuValValGlu 136

QY 634 CTGTCAGCTACTGCTGTGATATCCCTGGCATTTGGACGTACATTCTGGAACCATTTT 693
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
137 ProThrGlyGlnAlaIleIleAlaIleThrPheAlaAsnTyrIleIleGlnProSerPhe 156

QY 694 ATTCAATGTGAAATCCCTGAACCTTGCATCAAGTCACTACAGCTGTGGGCATAACTGTA 753
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 ProSerCysAspProProTyrLeuAlaCysArgLeuLeuAlaAlaCysIleCysLeu 176

QY 754 GTGATGGTCTCTAAATAGCATGAGTGTGAGCTGGAGCGCCGGATCCAGATTTTCTTAACC 813
Db      ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
177 LeuThrPheValAsnCysAlaTyrValLysTrpGlyThrArgValGlnAspThrPheThr 196

QY 814 TTTTGCAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATAAA 873
Db      ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
197 TyrAlaLysValValAlaLeuIleAlaIleIleValMetGlyLeuValLysLeuCysGln 216

QY 874 GGTCAAACGCAGAACTTTAAAGACGCCCTTTTTCAGGAAGAGATTCAAGTATTACCGCGTTG 933
Db      ||||| ::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
217 GlyHisSerGluHisPheGlnAspAlaPheGluGlySerSerTrpAspMetGlyAsnLeu 236

QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCACTTTGTT 993
Db      ||||| ||||| ::: ||||| ||||| ||||| ||||| ||||| |||||
237 SerLeuAlaLeuTyrSerAlaLeuPheSerTyrSerGlyTrpAspThrLeuAsnPheVal 256

QY 994 ACTGAAGAAGTAGAAACCCCTGAAAAAACCATTCCTTGCATATGTATATCCATGGCC 1053
Db      ||||| ||||| ::: ||||| ||||| ||||| ||||| ||||| |||||
257 ThrGluGluIleLysAsnProGluArgAsnLeuProLeuAlaIleGlyIleSerMetPro 276

QY 1054 ATTGTCACCATTTGGCTATGTGCTGACAAATGTGGCTACTTTACGACCATTAATGCTGAG 1113
Db      ||||| ||||| ::: ||||| ||||| ||||| ||||| ||||| |||||
277 IleValThrLeuIleTyrIleLeuThrAsnValAlaTyrTyrThrValLeuAsnIleSer 296

QY 1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGGCTACTGGGAAATTC 1173
Db      ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
297 AspValLeuSerSerAspAlaValAlaValThrPheAlaAspGlnThrPheGlyMetPhe 316

QY 1174 TCATTAGCAGTTCGATCTTTGTTGGCCCTCTCTGCTTTGGCTCCATGAACGGTGGTG 1233
Db      ||||| ::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
317 SerTrpThrIleProIleAlaValAlaLeuSerCysPheGlyGlyLeuAsnAlaSerIle 336
```


QY 1390 CTTTTGAATTTCTCTCAGTTTGGCAGGTGGCTTTTATTGGGTGGCAGTTGCTGGGCTG 1449
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 381 LeuileAsnTyrTyrSerPheSerTyrTrpPheValGlyLeuSerIleValGlyGln 400
QY 1450 ATTTATCTTCGATACAAATGCCAGATATGCATCGTCCTTTCAAGGTGCCACTGTTTCATC 1509
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 401 LeuTyrLeuArgTrpLysGluProAspArgProArgProLeuLysLeuSerValPhePhe 420
QY 1510 CCAGCTTTGTTTCTTCACATGCCCTCTTCATGGTTGGCTTCCCTCTCTATTCCGACCCA 1569
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 421 ProileValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAspThr 440
QY 1570 TTTAGTACAGGGATTGGCTTCGTCACTCTGACTGGAGTCCCTGCGTATTATCTCTTT 1629
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 441 IleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeuIle 460
QY 1630 ATT-----ATATGGACAAGAAACCCAGGTGGTTTAGAATAATGTACAGAGAAATAACC 1683
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 461 IleArgValProGluHisLysArgProLeuTyrLeuArgArgIleValGlySerAlaThr 480
QY 1684 AGAACAATTACAAATAATA---CTGGAAGTTGTACCAGAAGAAGAT 1725
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 481 ArgTyrLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 495

RESULT 12

US-10-163-866-42
; Sequence 42, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-42

Alignment Scores:
Pred. No.: 1-51e-97 Length: 511
Score: 1131.50 Matches: 214
Percent Similarity: 68.00% Conservative: 109
Best Local Similarity: 45.05% Mismatches: 149
Query Match: 27.46% Indels: 3
DB: 15 Gaps: 2

US-09-667-170A-440 (1-2239) x US-10-163-866-42 (1-511)

QY 310 GGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAAAGTCACCTTTACTG 369
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 21 GlyAspGlyAlaserProGlyProGluGlnValLysLeuLysLysGluIleSerLeuLeu 40
QY 370 AGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAAATCTTCATCTCTCCTAAG 429
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 41 AsnGlyValCysLeuIleValGlyAsnMetIleGlySerGlyIlePheValSerProLys 60
QY 430 GGC GTGTCCAGAACACGGCGGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGG 489
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
* 44

Db 61 GlyValLeuIleTyrSerAlaSerPheGlyLeuSerLeuValIleTyrAlaValGlyGly 80
QY 490 GTCCTGTCTACTATTGGAGCTTTTGTCTTATGCTGAATTTGGGAACAACACTATAAGAAATCT 549
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 81 LeuPheSerValPheGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleLysSer 100
QY 550 GGAGGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTC 609
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 101 GlyAlaSerTyrAlaTyrIleLeuGluAlaPheGlyGlyPheLeuAlaPheIleArgLeu 120
QY 610 TGGGTGGAACCTCCTCATATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGA 669
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 121 TrpThrSerLeuLeuIleIleGluProThrSerGlnAlaIleIleAlaIleThrPheAla 140
QY 670 CGCTACATTTCTGGAAACCATTTTATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTC 729
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 141 AsnTyrMetValGlnProLeuPheProSerCysPheAlaProTyrAlaAlaSerArgLeu 160
QY 730 ATTACAGCTGTGGGCATAACTGTAGTAGTGATGCTCTAAATAGCATGAGTGTAGCTGGAGC 789
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 161 LeuAlaAlaAlaCysIleCysLeuLeuThrPheIleAsnCysAlaTyrValLysTrpGly 180
QY 790 GCCCGGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATAATTATAGTC 849
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 181 ThrLeuValGlnAspIlePheThrTyrAlaLysValLeuAlaLeuIleAlaValIleVal 200
QY 850 CCTGGAGTTATGCAGCTAAATTAAGGTCAAACGCAGAACTTTAAAGACGCCTTTTCAGGA 909
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 201 AlaGlyIleValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGluGly 220
QY 910 AGAGATTCAAGTATTACGCGGTTGCCACTGCTGCTTTTATTATGGAATGTATGCATATGCT 969
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240
QY 970 GGCTGGTTTTTACCTCAACTTTGTTACTGAAGAAGTAGAAACCCCTGAAAAAACCATTTCCC 1029
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 241 GlyTrpAspThrLeuAsnTyrValThrGluGluIleLysAsnProGluArgAsnLeuPro 260
QY 1030 CTTTGAATATGTATATCCATGGCCATTGTACCATTTGGCTATGTGTGACAAATGTGGCC 1089
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 261 LeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeuThrAsnValAla 280
QY 1090 TACTTTACGACCAATTAATGTCTGAGGAGCTGCTGCTTTTCAAATGCAGTGGCAGTGACCTTT 1149
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 281 TyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThrPhe 300
QY 1150 TCTGAGCGGCTACTGGGAAATTTCTCATTAGCAGTTCGATCTTTTGTGCTCTCCTGC 1209
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 301 AlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerValAlaLeuSerCys 320
QY 1210 TTTGGCTCCATGAACGGTGGTGTGTTTGTGCTCTCCAGTTTATTCTATGTTGCTCTCGA 1269
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 321 PheGlyGlyLeuAsnAlaSerIleValAlaAlaSerArgLeuPhePheValGlySerArg 340
QY 1270 GAGGTCACCTTCCAGAAATCCTCTCCATGATTTCATGTCGCGCAAGCACACTCCTCTACCA 1329
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 341 GluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPheThrProValPro 360
QY 1330 GCTGTTATTGTTTGCACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGACCTCGACAGT 1389
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 361 SerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePheGln 380
QY 1390 CTTTTGAATTTCTCAGTTTTCAGGTGGCTTTTATTGGGTGGCAGTTGCTGGGCTG 1449
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 381 LeuileAsnTyrTyrSerPheSerTyrTrpPheValGlyLeuSerIleValGlyGln 400
QY 1450 ATTTATCTTCGATACAAATGCCAGATATGCATCGCTCTTCAAGGTGCCACTGTTTCATC 1509
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 401 LeuTyrLeuArgTrpLysGluProAspArgProArgProLeuLysLeuSerValPhePhe 420
QY 1510 CCAGCTTTGTTTCTCTTCACATGCCCTCTTCATGTTGCCCTTTTCCCTCTATTCGGACCCA 1569
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 421 ProileValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAspThr 440

QY 1570 TTAGTACAGGATTGGCTTCGTCACTCACTCTGACTGGAGTCCCTGCGTATTATCTCTTT 1629
Db : : : : :
Db 441 IleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeuIle 460
QY 1630 ATT-----ATATGGGACAAAGAACCCAGGTGGTGTAGAAATAATGTCAGAGAAAATAACC 1683
Db : : : : :
Db 461 IleArgValProGluHisLysArgProLeuTyrLeuArgArgIleValGlySerAlaThr 480
QY 1684 AGAATACATAATAATA---CTGGAAGTTGTACCAGAAAGAGAT 1725
Db : : : : :
Db 481 ArgTyrLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 495
RESULT 13
US-10-214-867A-11
; Sequence 11, Application US/10214867A
; Publication No. US2003014844A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-214-867A-11
Alignment Scores:
Pred. No.: 1.16e-95 Length: 511
Score: 1111.50 Matches: 212
Percent Similarity: 67.58% Conservative: 109
Best Local Similarity: 44.63% Mismatches: 151
Query Match: Indels: 3
DB: Gaps: 2
US-09-667-170A-440 (1-2239) x US-10-214-867A-11 (1-511)
QY 310 GGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGAGAAAGTCACCTTACTG 369
Db : : : : :
Db 21 GlyAspGlyAlaSerProGlyProGluGlnValLysLeuLysLysGluIleSerLeuLeu 40
QY 370 AGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTCATCTCTCCTAAG 429
Db : : : : :
Db 41 AsnGlyValCysLeuIleValGlyAsnMetIleGlySerGlyIlePheValSerProLys 60
QY 430 GCGGTGCTCCAGAAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGG 489
Db : : : : :
Db 61 GlyValLeuIleTyrSerAlaSerPheGlyLeuSerLeuValIleTrpAlaValGlyGly 80
QY 490 GTCCTGTCACTATTGGAGCTTTGTCTTATGCTGAATTTGGGAACAACACTATAAGAAATCT 549
Db : : : : :
Db 81 LeuPheSerValPheGlyAlaLeuCysTyrAlaGluLeuGlyThrThrIleLysLysSer 100
QY 550 GGAGGTCATTACACATATATTTTGGAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTC 609
Db : : : : :
Db 101 GlyAlaSerTyrAlaTyrIleLeuGluAlaPheGlyPheLeuAlaPheIleArgLeu 120
QY 610 TGGGTGGAACCTCCTCATAATACGCCCTGACGTACTGCTGTGATATCCCTGGCATTGTGA 669
Db : : : : :
Db 121 TrpThrSerLeuLeuIleIleGluProThrSerGlnAlaIleIleAlaIleThrPheAla 140
QY 670 CGCTACATTCTGGAACCATTTTTTATTCAATGTGAAATCCCTGAACCTTGGATCGAGCTC 729

Db 141 AsnTyrMetValGlnPheLeuPheProSerCysPheAlaProTyrAlaAlaSerArgLeu 160
QY 730 ATTACAGCTGTGGGCATAAAGTGTAGTGTGCTTAAATAGCATGAGTGTGAGTGTGAGC 789
Db : : : : :
Db 161 LeuAlaAlaAlaCysIleCysLeuLeuThrPheIleAsnCysAlaTyrValLysTrpGly 180
QY 790 GCCCGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATTTCTGATAATTATAGTC 849
Db : : : : :
Db 181 ThrLeuValGlnAspIlePheThrTyrAlaLysValLeuAlaLeuIleAlaValIleVal 200
QY 850 CCTGGAGTTATGCAGCTAATTAAGGTCAAACGCAGAACTTTAAAGACGCTTTTTCAGGA 909
Db : : : : :
Db 201 AlaGlyIleValArgLeuGlyGlnGlyAlaSerThrHisPheGluAsnSerPheGluGly 220
QY 910 AGAGATTCAAGTATTACGCGGTGGCCACTGGCTTTTATTTATGGAATGTATGCATATGCT 969
Db : : : : :
Db 221 SerSerPheAlaValGlyAspIleAlaLeuAlaLeuTyrSerAlaLeuPheSerTyrSer 240
QY 970 GCGTGGTTTTACCTCAACTTGTACTGAAGAGTAGAAAAACCCCTGAAAAAACCATTCCT 1029
Db : : : : :
Db 241 GlyTrpAspThrLeuAsnTyrValThrGluGluIleLysAsnProGluArgAsnLeuPro 260
QY 1030 CTTGCAATATGATATCCATGGCCATTGTCCACTGGCTTTTCAAAATGCAGTGGCAGTTCCT 1089
Db : : : : :
Db 261 LeuSerIleGlyIleSerMetProIleValThrIleIleTyrIleLeuThrAsnValAla 280
QY 1090 TACTTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAAATGCAGTGGCAGTTCCTTT 1149
Db : : : : :
Db 281 TyrTyrThrValLeuAspMetArgAspIleLeuAlaSerAspAlaValAlaValThrPhe 300
QY 1150 TCTGAGCGGCTACTGGGAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCTCTCCTGC 1209
Db : : : : :
Db 301 AlaAspGlnIlePheGlyIlePheAsnTrpIleIleProLeuSerValAlaLeuSerCys 320
QY 1210 TTTGGCTCCATGAACGGTGGTGTGTTGTGCTCTCCAGTTATTCTATGTTGCGTCTCGA 1269
Db : : : : :
Db 321 PheGlyGlyLeuAsnAlaSerIleValAlaAlaAlaSerArgLeuPheValGlySerArg 340
QY 1270 GAGGTCACCTTCCAGAAATCTCTCCATGATTATGTCGCGCAAGCACACTCCTCTACCA 1329
Db : : : : :
Db 341 GluGlyHisLeuProAspAlaIleCysMetIleHisValGluArgPheThrProValPro 360
QY 1330 GCTGTATTGTTTGCACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGACCTCGACAGT 1389
Db : : : : :
Db 361 SerLeuLeuPheAsnGlyIleMetAlaLeuIleTyrLeuCysValGluAspIlePheGln 380
QY 1390 CTTTGTGAATTTCCCTCAGTTTTCAGGTGGCTTTTATTTGGCTGGCAGTTGCTGGGCTG 1449
Db : : : : :
Db 381 LeuIleAsnTyrTyrSerPheSerTyrTrpPhePheValGlyLeuSerIleValGlyGln 400
QY 1450 ATTATCTTCGATACAAATGCCAGATATGCATCGTCTTCAAGGTGCCACTGTTTCATC 1509
Db : : : : :
Db 401 LeuTyrLeuArgTrpLysGluProCysArgProArgProLeuLysLeuSerValPhePhe 420
QY 1510 CCAGCTTTGTTTCCCTTCATGCTCTTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCA 1569
Db : : : : :
Db 421 ProIleValPheCysLeuCysThrIlePheLeuValAlaValProLeuTyrSerAspThr 440
QY 1570 TTAGTACAGGATTGGCTTCGTCTCATCTCATCTGACTGGAGTCCCTGCGTATTATCTCTTT 1629
Db : : : : :
Db 441 IleAsnSerLeuIleGlyIleAlaIleAlaLeuSerGlyLeuProPheTyrPheLeuIle 460
QY 1630 ATT-----ATATGGGACAAAGAAACCCAGGTGGTGTAGAAATAATGTACAGAAAAATAACC 1683
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Db 481 ArgTyrLeuGlnValLeuCysMetSerValAlaAlaGluMetAsp 495
RESULT 14
US-10-163-866-43

; Sequence 43, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-43

Alignment Scores:
Pred. No.: 1,03e-94 Length: 535
Score: 1101.50 Matches: 220
Percent Similarity: 65.52% Conservative: 103
Best Local Similarity: 44.62% Mismatches: 161
Query Match: 26.74% Indels: 9
DB: 15 Gaps: 4

US-09-667-170A-440 (1-2239) x US-10-163-866-43 (1-535)

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QY 382 ATTATCATTTGGACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGTCTCCAG 441
Db 48 IleIleValGlyAsnIleIleGlySerGlyIlePheValSerProLysSerGlyValLeuGlu 67
QY 442 AACACGGGCAGCGTGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCACTA 501
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QY 502 TTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACATAAAGAAATCTGGAGGTCAATTAC 561
Db 88 ValGlyAlaLeuCysTyrAlaGluLeuGlyValThrIleProLysSerGlyGlyAspTyr 107
QY 562 ACATATATTTTGAAGTCTTTTGGTCCATTACCACTTTGTACGAGTCTGGGTGGAATC 621
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QY 622 CTCATAATACGCCCTGCAGCTACTGTGTGATATCCCTGGCATTTGGACGCTACATTCTG 681
Db 128 LeuValIleTyrProThrAsnGlnAlaValIleAlaLeuThrPheSerAsnTyrValLeu 147
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Db 168 CysLeuLeuLeuLeuThrTrpValAsnCysSerSerValArgTrpAlaThrArgValGln 187
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QY 973 TGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTCCTT 1032
Db 248 TrpAsnPheLeuAsnTyrValThrGluLeuValAspProTyrLysAsnLeuProArg 267
QY 1033 GCAATATGTATATCCATGGCCATTGTCCACCATTTGGCTATGTGCTGACAAATGTGGCCTAC 1092
Db 268 AlaIlePheIleSerIleProLeuValThrPheValTyrValPheAlaAsnValAlaTyr 287
QY 1093 TTTACGACCATTAATGCTGAGGAGCTGCTGCTTTCAAATGCGAGTGGCAGTGACCTTTTCT 1152
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QY 1153 GAGCGCTACTGGGAAATTTCTCATTAGCAGTTCCGATCTTTGTTGCCCCCTCTCCTGCTTT 1212
Db 308 GluLysLeuLeuGlyValMetAlaTrpIleMetProIleSerValAlaLeuSerThrPhe 327
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Db 468 TyrTrpGlnHisLysProLysCysPheSerAspPheIleGluLeuLeuThrLeuValSer 487
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RESULT 15
US-10-163-866-44
; Sequence 44, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05

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; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-163-866-44

Alignment Scores:
Pred. No.:      1.03e-94      Length:      535
Score:          1101.50      Matches:      220
Percent Similarity: 65.52%      Conservative: 103
Best Local Similarity: 44.62%      Mismatches:   161
Query Match:     26.74%      Indels:       9
DB:              15          Gaps:          4

US-09-667-170A-440 (1-2239) x US-10-163-866-44 (1-535)

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QY 322 TTTTCAGGAAGAGAGAAAGTGCAGCTGAAGAGGAAAGTCACCTTTACTGAGGGGAGTCTCC 381
Db 28 GlySerGlyGlyGlyValAlaLeuLysLysGluIleGlyLeuValSerAlaCysGly 47

QY 382 ATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAAGGCGTGTCCAG 441
Db 48 IleIleValGlyAsnIleIleGlySerGlyIlePheValSerProLysGlyValLeuGlu 67

QY 442 AACACGGGACGCTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTA 501
Db 68 AsnAlaGlySerValGlyLeuAlaLeuIleValTrpIleValThrGlyPheIleThrVal 87

QY 502 TTTGGAGCTTTGTCTTATGCTGAATTGGGAACAACACTATAAAGAAATCTGGAGGTCATTAC 561
Db 88 ValGlyAlaLeuCysTyrAlaGluLeuGlyValThrIleProLysSerGlyGlyAspTyr 107

QY 562 ACATATATTTTGGAGTCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGTGGAACTC 621
Db 108 SerTyrValLysAspIlePheGlyGlyLeuAlaGlyPheLeuArgLeuTrpIleAlaVal 127

QY 622 CTCATAATACGCCCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTCTG 681
Db 128 LeuValIleTyrProThrAsnGlnAlaValIleAlaLeuThrPheSerAsnTyrValLeu 147

QY 682 GAACCATTTTATTCAATGTGAAATCCCTGAACCTTGGCATCAAGCTCATTACAGCTGTG 741
Db 148 GlnProLeuPheProThrCysPheProProGluSerGlyLeuArgLeuLeuAlaIle 167

QY 742 GGCATAACTGTAGTGGTCCTTAAATAGCATGATGTGCTGAGCTGGAGCGCCCGGATCCAG 801
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QY 802 ATTTTCTTAACCTTTTGCAGGCTCACAGCAATCTTGATAATTATAGTCCCTGGAGTTATG 861
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Db 208 GlnIleCysLysGlyGluTyrPheTrpLeuGluProLysAsnAlaPheGluAsnPheGln 227

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QY 1633 ATATGGACAAAGAAACCCAGGTGGTTTAGAATAATGTTCAGAGAAAAATAACAGAACATTA 1692
Db 468 TyrTrpGlnHisLysProLysCysPheSerAspPheIleGluLeuLeuThrLeuValSer 487
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Db 488 GlnLysMetCysValValValTyrProGluValGluArg 500
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Search completed: October 31, 2003, 11:39:13
Job time : 231 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2003, 07:20:58 ; Search time 114 Seconds
(without alignments)
8668.920 Million cell updates/sec

Title: US-09-667-170A-440
Perfect score: 2239
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0
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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	24	1.1	40000	4	US-09-780-049-18
C 5	24	1.1	162450	4	US-09-345-882-1
C 6	23	1.0	72928	3	US-09-009-913-1
7	22	1.0	333	3	US-09-018-584A-27
8	22	1.0	350	2	US-08-623-906A-17
9	22	1.0	11288	3	US-08-646-301A-1
10	22	1.0	11288	4	US-08-481-968A-4
11	22	1.0	11288	4	US-08-154-712B-4
12	22	1.0	15056	4	US-09-474-699-10
13	22	1.0	36651	4	US-09-738-894A-3
14	22	1.0	36651	4	US-09-964-469-3
C 15	22	1.0	38653	4	US-09-922-445-1
16	22	1.0	64467	4	US-09-803-671B-3
17	22	1.0	246240	2	US-08-724-394A-20
18	22	1.0	246240	2	US-08-724-394A-21
19	22	1.0	246240	2	US-08-724-394A-22
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23	21	0.9	668	3	US-09-328-111-687
24	21	0.9	704	3	US-09-475-316A-26
25	21	0.9	913	4	US-09-620-312D-819
26	21	0.9	950	3	US-08-984-550-1
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30	21	0.9	1880	4	US-09-620-312D-897	Sequence 897, App
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C 45	20	0.9	535	4	US-09-736-457-992	Sequence 992, App
46	20	0.9	551	4	US-09-702-705-1105	Sequence 1105, Ap
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101	20	0.9	22481	5	PCT-US95-07201-43	Sequence 43, Appl	174	19	0.8	1347	4	US-09-165-922A-11	Sequence 11, Appl
102	20	0.9	22484	4	US-09-875-223-2	Sequence 2, Appl	c 175	19	0.8	1361	4	US-09-489-847-64	Sequence 64, Appl
103	20	0.9	26000	4	US-09-843-376-10	Sequence 10, Appl	c 176	19	0.8	1381	2	US-08-454-557C-49	Sequence 49, Appl
c 104	20	0.9	45716	4	US-08-965-048-5	Sequence 5, Appl	c 177	19	0.8	1381	2	US-08-340-426D-49	Sequence 49, Appl
c 105	20	0.9	45989	4	US-08-965-048-6	Sequence 6, Appl	c 178	19	0.8	1381	2	US-08-450-673C-49	Sequence 49, Appl
106	20	0.9	46718	4	US-09-816-093-3	Sequence 3, Appl	c 179	19	0.8	1381	5	PCT-US95-17111A-49	Sequence 49, Appl
107	20	0.9	51719	4	US-09-918-686-2	Sequence 2, Appl	c 180	19	0.8	1448	4	US-09-625-040-1	Sequence 1, Appl
c 108	20	0.9	55298	4	US-09-491-356C-1	Sequence 1, Appl	181	19	0.8	1450	1	US-08-686-178-1	Sequence 1, Appl
c 109	20	0.9	64467	4	US-09-803-671B-3	Sequence 3, Appl	182	19	0.8	1568	3	US-09-043-937A-1	Sequence 1, Appl
c 110	20	0.9	70000	4	US-09-851-896-3	Sequence 3, Appl	c 183	19	0.8	1589	1	US-07-971-092-1	Sequence 1, Appl
c 111	20	0.9	72604	4	US-09-268-992-7	Sequence 7, Appl	184	19	0.8	1600	2	US-08-487-113D-117	Sequence 117, App
c 112	20	0.9	72604	4	US-09-657-474-7	Sequence 7, Appl	185	19	0.8	1600	2	US-08-720-420A-117	Sequence 117, App
c 113	20	0.9	74962	4	US-09-685-853A-3	Sequence 3, Appl	c 186	19	0.8	1611	6	5198342-1	Patent No. 5198342
114	20	0.9	92139	4	US-09-918-686-1	Sequence 1, Appl	187	19	0.8	1656	4	US-09-904-615-27	Sequence 27, Appl
c 115	20	0.9	98844	4	US-09-791-211-10	Sequence 10, Appl	188	19	0.8	1781	4	US-09-040-229B-3	Sequence 3, Appl
c 116	20	0.9	99500	4	US-09-798-096-10	Sequence 10, Appl	189	19	0.8	1834	1	US-08-297-633A-1	Sequence 1, Appl
c 117	20	0.9	116592	4	US-09-818-512-3	Sequence 3, Appl	190	19	0.8	1834	1	US-08-485-721-8	Sequence 8, Appl
c 118	20	0.9	148567	4	US-09-801-876B-3	Sequence 3, Appl	191	19	0.8	1834	2	US-08-392-935-8	Sequence 8, Appl
119	20	0.9	162450	4	US-09-345-882-1	Sequence 1, Appl	192	19	0.8	1834	5	PCT-US93-08325-1	Sequence 1, Appl
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c 122	20	0.9	246240	2	US-08-724-394A-22	Sequence 22, Appl	195	19	0.8	1894	1	US-08-615-170-20	Sequence 20, Appl
123	19	0.8	36	1	US-08-113-646A-6	Sequence 6, Appl	196	19	0.8	1897	1	US-08-615-170-18	Sequence 18, Appl
124	19	0.8	113	1	US-08-120-827-98	Sequence 98, Appl	197	19	0.8	1897	2	US-08-809-494A-1	Sequence 1, Appl
125	19	0.8	113	1	US-08-478-675-98	Sequence 98, Appl	198	19	0.8	1897	3	US-09-352-302-1	Sequence 1, Appl
c 126	19	0.8	192	3	US-09-157-177-115	Sequence 115, App	199	19	0.8	1901	3	US-09-338-907-181	Sequence 181, App
c 127	19	0.8	249	3	US-09-103-875-13	Sequence 13, Appl	200	19	0.8	1901	4	US-09-218-207-181	Sequence 181, App
128	19	0.8	291	1	US-07-922-723A-7	Sequence 7, Appl	201	19	0.8	1906	2	US-08-809-494A-3	Sequence 3, Appl
129	19	0.8	291	1	US-07-799-828C-7	Sequence 7, Appl	202	19	0.8	1906	3	US-09-352-302-3	Sequence 3, Appl
130	19	0.8	291	1	US-08-074-275-7	Sequence 7, Appl	203	19	0.8	1922	1	US-08-700-749A-7	Sequence 7, Appl
131	19	0.8	291	1	US-08-480-366-7	Sequence 7, Appl	204	19	0.8	1922	3	US-09-020-684-7	Sequence 7, Appl
132	19	0.8	291	2	US-07-952-277A-7	Sequence 7, Appl	205	19	0.8	1922	3	US-09-020-467-7	Sequence 7, Appl
133	19	0.8	344	2	US-08-623-906A-8	Sequence 8, Appl	206	19	0.8	1922	3	US-09-020-685-7	Sequence 7, Appl
134	19	0.8	415	3	US-09-018-584A-18	Sequence 18, Appl	207	19	0.8	1922	3	US-09-020-683-7	Sequence 7, Appl
c 135	19	0.8	428	4	US-09-495-050A-101	Sequence 101, App	208	19	0.8	1938	1	US-08-278-635B-1	Sequence 1, Appl
136	19	0.8	454	2	US-08-623-906A-6	Sequence 6, Appl	209	19	0.8	1938	3	US-08-464-258B-1	Sequence 1, Appl
137	19	0.8	517	4	US-09-482-273-45	Sequence 45, Appl	210	19	0.8	1938	3	US-08-471-961-1	Sequence 1, Appl
138	19	0.8	540	4	US-09-313-434C-15	Sequence 15, Appl	211	19	0.8	1991	2	US-08-415-593-40	Sequence 40, Appl
139	19	0.8	561	4	US-09-404-879A-50	Sequence 50, Appl	212	19	0.8	2031	4	US-08-706-054A-1	Sequence 1, Appl
140	19	0.8	561	4	US-09-338-933-50	Sequence 50, Appl	c 213	19	0.8	2031	4	US-08-706-054A-2	Sequence 2, Appl
141	19	0.8	561	4	US-09-215-681-50	Sequence 50, Appl	214	19	0.8	2031	4	US-09-313-299-1	Sequence 1, Appl
c 142	19	0.8	618	3	US-08-961-810-17	Sequence 17, Appl	c 215	19	0.8	2031	4	US-09-313-299-2	Sequence 2, Appl
c 143	19	0.8	618	3	US-08-352-902D-17	Sequence 17, Appl	216	19	0.8	2133	3	US-08-808-032-1	Sequence 1, Appl
c 144	19	0.8	618	4	US-09-265-503B-17	Sequence 17, Appl	217	19	0.8	2160	2	US-08-902-853-4	Sequence 4, Appl
145	19	0.8	672	1	US-07-847-010-21	Sequence 21, Appl	218	19	0.8	2178	3	US-08-781-891-72	Sequence 72, Appl
146	19	0.8	685	4	US-09-183-266A-16	Sequence 16, Appl	219	19	0.8	2178	4	US-09-618-166-72	Sequence 72, Appl
147	19	0.8	689	4	US-09-325-932A-10	Sequence 10, Appl	c 220	19	0.8	2233	1	US-08-129-129-2	Sequence 2, Appl
148	19	0.8	758	3	US-08-906-616-126	Sequence 126, App	c 221	19	0.8	2280	4	US-09-346-408-3	Sequence 3, Appl
149	19	0.8	758	3	US-08-906-616-126	Sequence 126, App	222	19	0.8	2320	4	US-09-813-817-1	Sequence 1, Appl
150	19	0.8	758	3	US-08-639-075A-126	Sequence 126, App	223	19	0.8	2320	4	US-09-978-197-1	Sequence 1, Appl
151	19	0.8	758	3	US-09-012-431-126	Sequence 126, App	c 224	19	0.8	2336	1	US-08-247-946A-1	Sequence 1, Appl
152	19	0.8	758	3	US-09-012-692-126	Sequence 126, App	c 225	19	0.8	2336	5	PCT-US95-06420-1	Sequence 1, Appl
153	19	0.8	758	3	US-08-906-613-126	Sequence 126, App	226	19	0.8	2457	4	US-09-620-312D-223	Sequence 223, App
154	19	0.8	787	4	US-09-620-312D-444	Sequence 444, App	227	19	0.8	2555	2	US-08-693-457-3	Sequence 3, Appl
155	19	0.8	798	4	US-09-257-179-38	Sequence 38, Appl	228	19	0.8	2555	3	US-09-265-731-3	Sequence 3, Appl
c 156	19	0.8	825	2	US-08-486-148B-1	Sequence 1, Appl	229	19	0.8	2566	4	US-09-594-506-33	Sequence 33, Appl
157	19	0.8	843	4	US-09-130-491-11	Sequence 11, Appl	230	19	0.8	2634	2	US-08-818-514-1	Sequence 1, Appl
158	19	0.8	936	2	US-08-557-309B-21	Sequence 21, Appl	c 231	19	0.8	2634	2	US-08-818-514-2	Sequence 2, Appl
159	19	0.8	936	3	US-08-834-306-21	Sequence 21, Appl	232	19	0.8	2634	3	US-09-115-934A-1	Sequence 1, Appl
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162	19	0.8	959	4	US-09-205-258-19	Sequence 19, Appl	c 235	19	0.8	2634	4	US-09-611-175-2	Sequence 2, Appl
163	19	0.8	1001	4	US-09-641-638-208	Sequence 208, App	c 236	19	0.8	2791	4	US-09-570-367C-1	Sequence 1, Appl
c 164	19	0.8	1001	4	US-09-641-638-292	Sequence 292, App	c 237	19	0.8	2882	1	US-08-393-219-2	Sequence 2, Appl
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172	19	0.8	1312	3	US-09-262-653A-9	Sequence 9, Appl	245	19	0.8	3647	3	US-09-360-197-7	Sequence 7, Appl
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C 394	19	0.8	152331	3	US-09-128-155-16	Sequence 16, Appl	467	18	0.8	613	4	US-08-981-799A-47	Sequence 47, Appl
C 395	19	0.8	169998	4	US-09-676-610B-24	Sequence 24, Appl	C 468	18	0.8	617	3	US-09-385-982-222	Sequence 222, App
C 396	19	0.8	174493	4	US-09-804-471A-3	Sequence 3, Appli	469	18	0.8	629	2	US-08-698-805-3	Sequence 3, Appli
C 397	19	0.8	176373	3	US-09-128-155-17	Sequence 17, Appl	470	18	0.8	630	4	US-09-342-681C-5	Sequence 5, Appli
C 398	19	0.8	197496	4	US-09-877-177A-10	Sequence 10, Appl	471	18	0.8	642	4	US-09-288-143-35	Sequence 35, Appl
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c 5470 6 5196523-5 Patent No. 5196523
5578 1 US-08-081-610-2 Sequence 2, Appli
5613 2 US-08-463-418-1 Sequence 1, Appli
5687 2 US-08-380-403A-3 Sequence 3, Appli
5687 2 US-08-895-628-3 Sequence 3, Appli
5687 4 US-08-895-810D-3 Sequence 3, Appli
5720 4 US-09-442-100-1 Sequence 1, Appli
5720 4 US-08-939-106-1 Sequence 1, Appli
5847 4 US-09-920-672-10 Sequence 10, Appl
6138 3 US-09-067-800-4 Sequence 4, Appli
6138 4 US-09-349-677-4 Sequence 4, Appli
6356 4 US-09-770-595A-1 Sequence 1, Appli
6638 2 US-08-070-301-2 Sequence 2, Appli
6701 4 US-09-004-838-107 Sequence 107, App
6755 3 US-08-931-999-4 Sequence 4, Appli
7277 4 US-09-795-927-5 Sequence 5, Appli
7451 1 US-08-684-672-23 Sequence 23, Appl
7542 4 US-09-734-030-3 Sequence 3, Appli
7620 1 US-07-767-135-1 Sequence 1, Appli
7620 1 US-07-841-652-1 Sequence 1, Appli
7676 1 US-08-451-777A-7 Sequence 7, Appli
7676 2 US-08-451-778A-7 Sequence 7, Appli
7676 5 US-08-998-208-7 Sequence 7, Appli
7676 5 PCT-US95-06743-7 Sequence 7, Appli
7941 4 US-09-816-703A-1 Sequence 1, Appli
8083 3 US-09-383-630-4 Sequence 4, Appli
8083 3 US-09-383-630-5 Sequence 5, Appli
8982 3 US-08-976-255-5 Sequence 5, Appli
9299 3 US-08-458-434A-7 Sequence 7, Appli
9837 1 US-08-832-883-68 Sequence 68, Appl
9837 2 US-08-832-877-68 Sequence 68, Appl
9919 3 US-08-880-179-1 Sequence 1, Appli
10380 3 US-09-077-354B-3 Sequence 3, Appli
10640 4 US-09-417-485D-5 Sequence 5, Appli
10684 3 US-08-618-100B-3 Sequence 3, Appli
11464 3 US-08-884-324-13 Sequence 13, Appl
11721 4 US-09-026-039-3 Sequence 3, Appli
11721 4 US-09-026-039-3 Sequence 3, Appli

C 977 17 0.8 260 4 US-09-702-705-1208
C 978 17 0.8 260 4 US-09-736-457-1208
979 17 0.8 268 2 US-08-619-542B-27
980 17 0.8 278 4 US-09-370-838-159
981 17 0.8 279 2 US-08-623-906A-3
982 17 0.8 284 4 US-09-313-294A-1545
983 17 0.8 297 1 US-08-616-368A-17
984 17 0.8 297 3 US-09-054-298-17
985 17 0.8 297 3 US-08-818-655-17
986 17 0.8 297 4 US-09-305-839-17
987 17 0.8 299 2 US-08-623-906A-19
C 988 17 0.8 308 1 US-08-171-385-25
C 989 17 0.8 308 3 US-08-361-441B-25
990 17 0.8 319 2 US-08-244-537-11
991 17 0.8 322 4 US-09-495-050A-281
992 17 0.8 325 1 US-08-102-757-18
993 17 0.8 334 2 US-08-522-421-3
994 17 0.8 347 4 US-09-495-050A-188
995 17 0.8 349 1 US-07-603-451A-4
996 17 0.8 349 1 US-08-060-822A-4
997 17 0.8 349 5 PCT-US94-05257-4
998 17 0.8 350 1 US-08-248-016-11
999 17 0.8 350 1 US-08-451-501-11
1000 17 0.8 350 5 PCT-US95-06761-11

ALIGNMENTS

RESULT 1
US-08-861-549-2
; Sequence 2, Application US/08861549
; Patent No. 5874246
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW TRANSCRIPTION REPRESSOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,549
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0306 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 737 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 1620089

US-08-861-549-2
Query Match 1.2%; Score 27; DB 2; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2191 GAGGAGAGAGGTAGAGCTGTTCTTAA 2217
|||||
Db 711 GAGGAGAGAGGTAGAGCTGTTCTTAA 737
RESULT 2
US-09-016-434-252
; Sequence 252, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT13
; CLONE: 1620089
US-09-016-434-252

Query Match 1.2%; Score 27; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 GAGGAGAGAGGTAGAGCTGTTCTTAA 2217
|||||
Db 712 GAGGAGAGAGGTAGAGCTGTTCTTAA 738

RESULT 3
US-09-920-759-13
; Sequence 13, Application US/09920759
; Patent No. 6537811
; GENERAL INFORMATION:

APPLICANT: Brenda F. Baker
APPLICANT: Susan M. Preier
TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION
FILE REFERENCE: RTS-0267
CURRENT APPLICATION NUMBER: US/09/920,759
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 13
LENGTH: 15788
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 690
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 691
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 692
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 693
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NAME/KEY: unsure
LOCATION: 707
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 708
OTHER INFORMATION: unknown
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LOCATION: 709
OTHER INFORMATION: unknown
NAME/KEY: unsure

LOCATION: 710
OTHER INFORMATION: unknown
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LOCATION: 711
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 712
OTHER INFORMATION: unknown
NAME/KEY: unsure
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NAME/KEY: unsure
LOCATION: 731
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 732
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 734

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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 735
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 736
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 737
; OTHER INFORMATION: unknown
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
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; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 748
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 749
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 750
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 751
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Query Match      1.1%; Score 24; DB 4; Length 15788;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      27 CCAGCCTGGGTGACAGTGAGACTC 50
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Db      9784 CCAGCCTGGGTGACAGTGAGACTC 9807
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RESULT 4
US-09-780-049-18/c
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
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; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18
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Query Match      1.1%; Score 24; DB 4; Length 40000;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      27 CCAGCCTGGGTGACAGTGAGACTC 50
      |||||
Db      15461 CCAGCCTGGGTGACAGTGAGACTC 15438
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RESULT 5
US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: GENSET.031A
; CURRENT APPLICATION NUMBER: US/09/345,882
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 162450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 72794
; OTHER INFORMATION: 5-124-273 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 88073
; OTHER INFORMATION: 5-127-261 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 90842
; OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 93714
; OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97122
; OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 97152
; OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99098
; OTHER INFORMATION: 5-130-257 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 99117
; OTHER INFORMATION: 5-130-276 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 103806
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OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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NAME/KEY: allele
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OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
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Query Match 1.1%; Score 24; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 CCAGCCTGGGTGACAGTGAGACTC 50
|||||
DB 54003 CCAGCCTGGGTGACAGTGAGACTC 53980

RESULT 6
US-09-009-913-1/c
; Sequence 1, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axys Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 72928 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-009-913-1

Query Match 1.0%; Score 23; DB 3; Length 72928;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTTGAAGTGAGCAGAGATCA 24
|||||
DB 47805 GAGGTTGAAGTGAGCAGAGATCA 47783

RESULT 7
US-09-018-584A-27
; Sequence 27, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; TITLE OF INVENTION: REPEAT DNA MARKERS

; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; LIBRARY: plasmid, pGem3Zf(+)
; CLONE: G539
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 15q26.2
US-09-018-584A-27

Query Match 1.0%; Score 22; DB 3; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 AAAAAAGAAAGAAAAAAGA 92
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DB 58 AAAAAAGAAAGAAAAAAGA 79

RESULT 8
US-08-623-906A-17
; Sequence 17, Application US/08623906A
; Patent No. 5874217
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Tamara
; APPLICANT: Dvorak, Jan
; APPLICANT: Halverson, Joy
; TITLE OF INVENTION: Microsatellite Sequences for Canine
; TITLE OF INVENTION: Genotyping
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HORHACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,906A

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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J.
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: A-62282/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..109
; OTHER INFORMATION: /note= "Nucleotides 1-109 are
; OTHER INFORMATION: unique flanking sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 110..195
; OTHER INFORMATION: /note= "Nucleotides 110-195 are
; OTHER INFORMATION: repeat sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 196..350
; OTHER INFORMATION: /note= "Nucleotides 196-350 are
; OTHER INFORMATION: unique flanking sequence"
US-08-623-906A-17
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Query Match 1.0%; Score 22; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 AAAAAGAAAGAAAGAAAAAGA 92
|||||
Db 121 AAAAAGAAAGAAAGAAAAAGA 142

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RESULT 9
US-08-646-301A-1
; Sequence 1, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-646-301A-1
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US-08-481-968A-4
; Sequence 4, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (CI
; TITLE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-481-968A-4
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; Sequence 4, Application US/08154712B
; Patent No. 6337209
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Re
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: PB1087US3
; CURRENT APPLICATION NUMBER: US/08/154,712B
; CURRENT FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
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; ORGANISM: Homo sapiens
US-08-154-712B-4
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Db 834 AAAAAGAAAGAAAGAAAAAGA 855

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RESULT 12
US-09-474-699-10
; Sequence 10, Application US/09474699
; Patent No. 6495130
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
; TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022001300
; CURRENT APPLICATION NUMBER: US/09/474,699
; CURRENT FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 60/114,262
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
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; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
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; CURRENT FILING DATE: 2000-12-18
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; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
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; CURRENT FILING DATE: 2001-09-28
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RESULT 15
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; Sequence 1, Application US/099222445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: GG126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
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; LOCATION: (31028)..(31747)
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7	1867	83.4	6080	14	US-10-144-649A-740 Sequence 740, App
8	1816	81.1	3144	14	US-10-163-866-31 Sequence 31, Appl
9	1722	76.9	2482	14	US-10-163-866-29 Sequence 29, Appl
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11	1600	71.5	2041	12	US-10-247-671-78 Sequence 78, Appl
12	1454	64.9	1861	14	US-10-163-866-30 Sequence 30, Appl
13	1420	63.4	1542	14	US-10-163-866-33 Sequence 33, Appl
14	1339	59.8	2000	14	US-10-163-866-34 Sequence 34, Appl
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C 99	24	1.1	579	13	US-10-027-632-65355	Sequence 65355, A	C 172	22	1.0	385	11	US-09-918-995-37276	Sequence 37276, A
C 100	24	1.1	579	13	US-10-027-632-65356	Sequence 65356, A	173	22	1.0	396	10	US-09-867-701-7510	Sequence 7510, Ap
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C 102	24	1.1	579	13	US-10-027-632-297204	Sequence 297204, A	C 175	22	1.0	417	12	US-09-814-353-9092	Sequence 9092, Ap
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C 106	24	1.1	657	13	US-10-027-632-258004	Sequence 258004, A	179	22	1.0	488	9	US-09-764-887-149	Sequence 149, App
C 107	24	1.1	741	13	US-10-027-632-11195	Sequence 11195, A	180	22	1.0	488	14	US-10-073-961-149	Sequence 149, App
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C 113	24	1.1	1398	10	US-09-764-877-2780	Sequence 2780, Ap	186	22	1.0	522	13	US-10-027-632-275106	Sequence 275106, A
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C 118	24	1.1	5377	11	US-09-764-891-9493	Sequence 9493, Ap	191	22	1.0	528	13	US-10-027-632-49852	Sequence 49852, A
C 119	24	1.1	6255	12	US-10-311-455-2002	Sequence 2002, Ap	C 192	22	1.0	545	10	US-09-962-832-13	Sequence 13, Appl
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C 137	23	1.0	633	13	US-10-027-632-61406	Sequence 61406, A	C 210	22	1.0	619	13	US-10-027-632-98723	Sequence 98723, A
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C 140	23	1.0	700	13	US-10-027-632-169649	Sequence 169649, A	C 213	22	1.0	625	13	US-10-027-632-115606	Sequence 115606, A
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C 146	23	1.0	810	13	US-10-027-632-169650	Sequence 169650, A	219	22	1.0	712	12	US-10-195-730-56	Sequence 56, Appl
C 147	23	1.0	832	14	US-10-198-846-6585	Sequence 6585, Ap	220	22	1.0	739	13	US-10-027-632-117462	Sequence 117462, A
C 148	23	1.0	900	13	US-10-027-632-173214	Sequence 173214, A	221	22	1.0	749	13	US-10-027-632-151116	Sequence 151116, A
C 149	23	1.0	900	13	US-10-027-632-173215	Sequence 173215, A	222	22	1.0	751	13	US-10-027-632-13694	Sequence 13694, A
C 150	23	1.0	956	13	US-10-027-632-129934	Sequence 129934, A	223	22	1.0	751	13	US-10-027-632-148380	Sequence 148380, A
C 151	23	1.0	1118	10	US-09-764-877-2777	Sequence 2777, Ap	224	22	1.0	751	13	US-10-027-632-148381	Sequence 148381, A
C 152	23	1.0	1815	11	US-09-822-846-60	Sequence 60, Appl	225	22	1.0	754	13	US-10-027-632-150424	Sequence 150424, A
C 153	23	1.0	2051	14	US-10-198-846-11396	Sequence 11396, A	226	22	1.0	754	13	US-10-027-632-150425	Sequence 150425, A
C 154	23	1.0	2361	9	US-09-925-302-281	Sequence 281, App	227	22	1.0	756	11	US-09-774-639-64	Sequence 64, Appl
C 155	23	1.0	2848	13	US-10-027-632-112062	Sequence 112062, A	228	22	1.0	756	11	US-09-969-730-99	Sequence 99, Appl
C 156	23	1.0	3109	11	US-09-746-783-85	Sequence 85, Appl	229	22	1.0	766	13	US-10-027-632-151678	Sequence 151678, A
C 157	23	1.0	4342	12	US-10-017-161-821	Sequence 821, App	C 230	22	1.0	766	13	US-10-027-632-151679	Sequence 151679, A
C 158	23	1.0	5958	12	US-10-311-455-1032	Sequence 1032, Ap	C 231	22	1.0	766	13	US-10-027-632-151680	Sequence 151680, A
C 159	23	1.0	7386	10	US-09-764-855-208	Sequence 208, App	C 232	22	1.0	767	13	US-10-027-632-149293	Sequence 149293, A
C 160	23	1.0	7386	14	US-10-072-349-208	Sequence 208, App	233	22	1.0	767	13	US-10-027-632-149294	Sequence 149294, A
C 161	23	1.0	10020	12	US-10-311-455-2265	Sequence 2265, Ap	234	22	1.0	812	13	US-10-027-632-161318	Sequence 161318, A
C 162	23	1.0	17216	10	US-09-764-877-3565	Sequence 3565, Ap	235	22	1.0	817	13	US-10-027-632-158769	Sequence 158769, A

C 236	22	1.0	827	13	US-10-027-632-161941	Sequence 161941,	C 309	22	1.0	22645	11	US-09-764-891-7673	Sequence 7673, Ap
237	22	1.0	879	13	US-10-027-632-101288	Sequence 101288,	C 310	22	1.0	22645	11	US-09-764-891-8183	Sequence 8183, Ap
238	22	1.0	879	13	US-10-027-632-101289	Sequence 101289,	C 311	22	1.0	25277	9	US-09-764-878-285	Sequence 285, App
239	22	1.0	1041	13	US-10-027-632-116643	Sequence 116643,	C 312	22	1.0	25277	9	US-09-764-860-1148	Sequence 1148, Ap
240	22	1.0	1041	13	US-10-027-632-116644	Sequence 116644,	C 313	22	1.0	25277	14	US-10-079-854-285	Sequence 285, App
241	22	1.0	1041	13	US-10-027-632-116645	Sequence 116645,	C 314	22	1.0	25277	14	US-10-074-095-1148	Sequence 1148, Ap
242	22	1.0	1043	13	US-10-027-632-116480	Sequence 116480,	C 315	22	1.0	25279	9	US-09-764-878-284	Sequence 284, App
243	22	1.0	1072	13	US-10-027-632-116539	Sequence 116539,	C 316	22	1.0	25279	9	US-09-764-860-1147	Sequence 1147, Ap
244	22	1.0	1072	13	US-10-027-632-116540	Sequence 116540,	C 317	22	1.0	25279	14	US-10-079-854-284	Sequence 284, App
245	22	1.0	1072	13	US-10-027-632-116541	Sequence 116541,	C 318	22	1.0	25279	14	US-10-074-095-1147	Sequence 1147, Ap
246	22	1.0	1128	13	US-10-027-632-31730	Sequence 31730, A	C 319	22	1.0	27062	11	US-09-764-891-8034	Sequence 8034, Ap
C 247	22	1.0	1131	13	US-10-027-632-264581	Sequence 264581,	C 320	22	1.0	31168	10	US-09-764-868-1464	Sequence 1464, Ap
C 248	22	1.0	1131	13	US-10-027-632-264582	Sequence 264582,	C 321	22	1.0	31994	9	US-09-764-860-599	Sequence 599, App
C 249	22	1.0	1475	12	US-10-261-078-3	Sequence 3, Appli	C 322	22	1.0	31994	10	US-09-764-904-71	Sequence 71, Appl
250	22	1.0	1556	13	US-10-027-632-256224	Sequence 256224,	C 323	22	1.0	31994	14	US-10-091-548-71	Sequence 71, Appl
C 251	22	1.0	1816	13	US-10-027-632-51324	Sequence 51324, A	C 324	22	1.0	31994	14	US-10-074-095-599	Sequence 599, App
C 252	22	1.0	1816	13	US-10-027-632-51325	Sequence 51325, A	C 325	22	1.0	32193	10	US-09-764-877-2147	Sequence 2147, Ap
C 253	22	1.0	1816	13	US-10-027-632-51326	Sequence 51326, A	C 326	22	1.0	32194	11	US-09-764-891-7028	Sequence 7028, Ap
C 254	22	1.0	1816	13	US-10-027-632-51327	Sequence 51327, A	C 327	22	1.0	36651	9	US-09-964-469-3	Sequence 3, Appli
255	22	1.0	2288	13	US-10-027-632-102001	Sequence 102001,	328	22	1.0	36651	12	US-10-425-962-3	Sequence 3, Appli
C 256	22	1.0	2325	13	US-10-027-632-103528	Sequence 103528,	329	22	1.0	41104	9	US-09-816-685-3	Sequence 3, Appli
C 257	22	1.0	2325	13	US-10-027-632-103529	Sequence 103529,	330	22	1.0	42863	12	US-10-017-161-1017	Sequence 1017, Ap
C 258	22	1.0	2384	13	US-10-027-632-111547	Sequence 111547,	C 331	22	1.0	46130	12	US-10-017-161-985	Sequence 985, App
C 259	22	1.0	2754	10	US-09-880-107-3720	Sequence 3720, Ap	C 332	22	1.0	50000	14	US-10-152-724A-21	Sequence 21, Appl
C 260	22	1.0	2921	14	US-10-198-846-11998	Sequence 11998, A	C 333	22	1.0	55611	12	US-10-017-161-783	Sequence 783, App
C 261	22	1.0	3233	10	US-09-964-824A-116	Sequence 116, App	C 334	22	1.0	63000	10	US-09-780-172-18	Sequence 18, Appl
C 262	22	1.0	3233	12	US-09-873-319-301	Sequence 301, App	335	22	1.0	64467	14	US-10-274-409-3	Sequence 3, Appli
C 263	22	1.0	3233	12	US-09-960-706-494	Sequence 494, App	336	22	1.0	65464	10	US-09-859-888-3	Sequence 3, Appli
C 264	22	1.0	3303	13	US-10-027-632-115241	Sequence 115241,	C 337	22	1.0	88191	10	US-09-799-799-3	Sequence 3, Appli
C 265	22	1.0	3303	13	US-10-027-632-115242	Sequence 115242,	338	22	1.0	99014	10	US-09-880-107-3428	Sequence 3428, Ap
266	22	1.0	3593	14	US-10-002-775-10	Sequence 10, Appl	339	22	1.0	113000	12	US-10-376-566-16	Sequence 16, Appl
267	22	1.0	3593	14	US-10-115-615-22	Sequence 22, Appl	340	22	1.0	113604	14	US-10-227-195A-1	Sequence 1, Appli
C 268	22	1.0	4203	11	US-09-764-891-7948	Sequence 7948, Ap	341	22	1.0	113604	14	US-10-227-195A-2	Sequence 2, Appli
269	22	1.0	4369	10	US-09-764-877-2824	Sequence 2824, Ap	342	22	1.0	118067	15	US-10-081-327-32	Sequence 32, Appl
270	22	1.0	5281	11	US-09-764-891-6949	Sequence 6949, Ap	343	22	1.0	161652	15	US-10-081-327-40	Sequence 40, Appl
271	22	1.0	5314	12	US-10-311-455-134	Sequence 134, App	344	22	1.0	167343	9	US-09-962-436-281	Sequence 281, App
272	22	1.0	5314	12	US-10-240-452-10	Sequence 10, Appl	345	22	1.0	167343	10	US-09-964-824A-273	Sequence 273, App
273	22	1.0	5586	12	US-10-311-455-621	Sequence 621, App	346	22	1.0	170834	9	US-09-835-232-7	Sequence 7, Appli
274	22	1.0	5744	10	US-09-764-847-1457	Sequence 1457, Ap	347	22	1.0	170834	12	US-10-308-485-7	Sequence 7, Appli
275	22	1.0	5744	14	US-10-092-154-1457	Sequence 1457, Ap	C 348	22	1.0	235033	14	US-10-301-844-1	Sequence 1, Appli
C 276	22	1.0	5986	12	US-10-311-455-2068	Sequence 2068, Ap	C 349	22	1.0	237326	14	US-10-301-844-2	Sequence 2, Appli
277	22	1.0	6012	12	US-10-240-453-211	Sequence 211, App	350	22	1.0	250000	12	US-10-225-810-26	Sequence 26, Appl
278	22	1.0	6020	12	US-10-204-708-8	Sequence 8, Appli	C 351	22	1.0	254366	11	US-09-822-871-3	Sequence 3, Appli
279	22	1.0	6020	12	US-10-311-455-172	Sequence 172, App	352	22	1.0	300000	14	US-10-262-552-33	Sequence 33, Appl
280	22	1.0	6103	12	US-10-311-455-2144	Sequence 2144, Ap	C 353	22	1.0	684973	10	US-09-263-959-1	Sequence 1, Appli
281	22	1.0	6195	12	US-10-311-455-564	Sequence 564, App	354	22	1.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
282	22	1.0	8404	12	US-10-311-455-1567	Sequence 1567, Ap	C 355	22	1.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
283	22	1.0	8677	10	US-09-764-877-3322	Sequence 3322, Ap	356	22	1.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
284	22	1.0	8680	10	US-09-764-877-3321	Sequence 3321, Ap	C 357	22	1.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
C 285	22	1.0	8866	12	US-10-240-453-154	Sequence 154, App	358	22	1.0	1503841	10	US-09-946-807-1	Sequence 1, Appli
C 286	22	1.0	8866	14	US-10-239-676-140	Sequence 140, App	C 359	22	1.0	1503841	10	US-09-946-807-1	Sequence 1, Appli
287	22	1.0	8962	12	US-10-311-455-660	Sequence 660, App	360	22	1.0	2940917	13	US-10-027-632-174763	Sequence 174763,
C 288	22	1.0	9372	10	US-09-764-877-3049	Sequence 3049, Ap	C 361	21	0.9	241	10	US-09-833-381-1089	Sequence 1089, Ap
C 289	22	1.0	9372	10	US-09-764-877-3244	Sequence 3244, Ap	362	21	0.9	273	11	US-09-764-891-7564	Sequence 7564, Ap
C 290	22	1.0	9723	12	US-10-311-455-2354	Sequence 2354, Ap	363	21	0.9	276	11	US-09-764-891-7561	Sequence 7561, Ap
291	22	1.0	9927	12	US-10-311-455-85	Sequence 85, Appl	C 364	21	0.9	283	10	US-09-917-800A-460	Sequence 460, App
292	22	1.0	10429	11	US-09-764-891-7375	Sequence 7375, Ap	C 365	21	0.9	284	12	US-09-814-353-17553	Sequence 17553, A
293	22	1.0	11288	9	US-09-947-925A-4	Sequence 4, Appli	C 366	21	0.9	326	12	US-09-814-353-18362	Sequence 18362, A
294	22	1.0	11288	10	US-09-822-634-1	Sequence 1, Appli	C 367	21	0.9	329	12	US-09-814-353-2705	Sequence 2705, Ap
295	22	1.0	11838	11	US-09-764-891-7020	Sequence 7020, Ap	C 368	21	0.9	329	12	US-09-814-353-9038	Sequence 9038, Ap
C 296	22	1.0	14410	11	US-09-764-891-8697	Sequence 8697, Ap	C 369	21	0.9	341	11	US-09-918-995-19067	Sequence 19067, A
C 297	22	1.0	14874	11	US-09-764-891-7672	Sequence 7672, Ap	C 370	21	0.9	349	12	US-09-814-353-18039	Sequence 18039, A
C 298	22	1.0	15002	11	US-09-770-107-3	Sequence 3, Appli	C 371	21	0.9	351	12	US-09-814-353-17579	Sequence 17579, A
299	22	1.0	15056	9	US-09-392-822-4	Sequence 4, Appli	372	21	0.9	353	11	US-09-918-995-17718	Sequence 17718, A
300	22	1.0	15056	11	US-09-814-357-14	Sequence 14, Appl	373	21	0.9	355	11	US-09-803-719-442	Sequence 442, App
301	22	1.0	15056	12	US-09-814-351-14	Sequence 14, Appl	C 374	21	0.9	376	9	US-09-770-791-249	Sequence 249, App
302	22	1.0	15056	14	US-10-045-116-25	Sequence 25, Appl	C 375	21	0.9	396	13	US-10-027-632-143615	Sequence 143615,
303	22	1.0	15056	14	US-10-226-820-10	Sequence 10, Appl	C 376	21	0.9	403	12	US-09-814-353-17949	Sequence 17949, A
C 304	22	1.0	16579	11	US-09-764-891-8443	Sequence 8443, Ap	377	21	0.9	405	11	US-09-918-995-37246	Sequence 37246, A
C 305	22	1.0	17252	9	US-09-764-860-1102	Sequence 1102, Ap	C 378	21	0.9	413	11	US-09-918-995-17359	Sequence 17359, A
C 306	22	1.0	17252	14	US-10-074-095-1102	Sequence 1102, Ap	379	21	0.9	424	11	US-09-918-995-16049	Sequence 16049, A
307	22	1.0	17993	10	US-09-768-781-5	Sequence 5, Appli	380	21	0.9	425	11	US-09-918-995-23485	Sequence 23485, A
C 308	22	1.0	22609	10	US-09-764-877-2146	Sequence 2146, Ap	381	21	0.9	427	11	US-09-918-995-17115	Sequence 17115, A

C 382	21	0.9	430	11	US-09-918-995-34700	Sequence 34700, A	455	21	0.9	599	14	US-10-313-542-236	Sequence 236, App
C 383	21	0.9	430	11	US-09-918-995-34846	Sequence 34846, A	456	21	0.9	611	13	US-10-027-632-204567	Sequence 204567,
384	21	0.9	451	9	US-09-864-761-5293	Sequence 5293, Ap	457	21	0.9	613	13	US-10-027-632-214800	Sequence 214800,
C 385	21	0.9	463	13	US-10-027-632-282957	Sequence 282957,	C 458	21	0.9	617	13	US-10-027-632-122200	Sequence 122200,
C 386	21	0.9	466	13	US-10-027-632-89647	Sequence 89647, A	C 459	21	0.9	618	13	US-10-027-632-96765	Sequence 96765, A
C 387	21	0.9	466	13	US-10-027-632-317215	Sequence 317215,	C 460	21	0.9	618	13	US-10-027-632-267651	Sequence 267651,
388	21	0.9	466	14	US-10-060-036-2357	Sequence 2357, Ap	C 461	21	0.9	618	13	US-10-027-632-308357	Sequence 308357,
C 389	21	0.9	472	11	US-09-918-995-12888	Sequence 12888, A	C 462	21	0.9	624	13	US-10-027-632-238994	Sequence 238994,
C 390	21	0.9	473	12	US-09-814-353-15422	Sequence 15422, A	463	21	0.9	624	13	US-10-027-632-238995	Sequence 238995,
C 391	21	0.9	476	11	US-09-918-995-20128	Sequence 20128, A	464	21	0.9	624	13	US-10-027-632-245434	Sequence 245434,
C 392	21	0.9	482	13	US-10-027-632-114819	Sequence 114819,	C 465	21	0.9	624	13	US-10-027-632-292776	Sequence 292776,
C 393	21	0.9	482	13	US-10-027-632-114820	Sequence 114820,	C 466	21	0.9	626	13	US-10-027-632-80782	Sequence 80782, A
C 394	21	0.9	486	13	US-10-027-632-135134	Sequence 135134,	C 467	21	0.9	632	13	US-10-027-632-277571	Sequence 277571,
C 395	21	0.9	488	11	US-09-918-995-4788	Sequence 4788, Ap	C 468	21	0.9	634	13	US-10-027-632-290545	Sequence 290545,
C 396	21	0.9	495	13	US-10-027-632-183036	Sequence 183036,	C 469	21	0.9	638	13	US-10-027-632-185104	Sequence 185104,
397	21	0.9	499	13	US-10-027-632-105984	Sequence 105984,	C 470	21	0.9	650	13	US-10-027-632-221216	Sequence 221216,
C 398	21	0.9	499	13	US-10-027-632-127943	Sequence 127943,	C 471	21	0.9	650	13	US-10-027-632-221217	Sequence 221217,
C 399	21	0.9	505	13	US-10-027-632-81648	Sequence 81648, A	C 472	21	0.9	656	13	US-10-027-632-275991	Sequence 275991,
C 400	21	0.9	505	13	US-10-027-632-292802	Sequence 292802,	C 473	21	0.9	657	13	US-10-027-632-275990	Sequence 275990,
C 401	21	0.9	506	11	US-09-770-961-295	Sequence 295, App	474	21	0.9	667	13	US-10-027-632-201563	Sequence 201563,
C 402	21	0.9	506	14	US-10-060-036-2005	Sequence 2005, Ap	C 475	21	0.9	668	10	US-09-879-536-687	Sequence 687, App
C 403	21	0.9	517	13	US-10-027-632-253113	Sequence 253113,	C 476	21	0.9	670	13	US-10-027-632-216727	Sequence 216727,
C 404	21	0.9	517	13	US-10-027-632-253114	Sequence 253114,	477	21	0.9	679	13	US-10-027-632-140340	Sequence 140340,
405	21	0.9	520	13	US-10-027-632-59434	Sequence 59434, A	478	21	0.9	687	14	US-10-106-698-1535	Sequence 1535, Ap
406	21	0.9	520	13	US-10-027-632-59435	Sequence 59435, A	479	21	0.9	689	13	US-10-027-632-18784	Sequence 18784, A
407	21	0.9	534	13	US-10-027-632-62213	Sequence 62213, A	C 480	21	0.9	697	13	US-10-027-632-18506	Sequence 18506, A
408	21	0.9	534	13	US-10-027-632-63102	Sequence 63102, A	C 481	21	0.9	697	13	US-10-027-632-38495	Sequence 38495, A
409	21	0.9	536	13	US-10-027-632-36732	Sequence 36732, A	482	21	0.9	716	13	US-10-027-632-18945	Sequence 18945, A
410	21	0.9	536	13	US-10-027-632-36733	Sequence 36733, A	483	21	0.9	721	13	US-10-027-632-149161	Sequence 149161,
C 411	21	0.9	539	13	US-10-027-632-37664	Sequence 37664, A	484	21	0.9	721	13	US-10-027-632-149162	Sequence 149162,
C 412	21	0.9	539	13	US-10-027-632-112677	Sequence 112677,	C 485	21	0.9	724	13	US-10-027-632-138318	Sequence 138318,
C 413	21	0.9	539	13	US-10-027-632-112678	Sequence 112678,	C 486	21	0.9	727	13	US-10-027-632-113907	Sequence 113907,
414	21	0.9	539	13	US-10-027-632-306523	Sequence 306523,	C 487	21	0.9	728	13	US-10-027-632-19831	Sequence 19831, A
415	21	0.9	546	13	US-10-027-632-5004	Sequence 5004, Ap	C 488	21	0.9	728	13	US-10-027-632-127549	Sequence 127549,
416	21	0.9	546	13	US-10-027-632-5005	Sequence 5005, Ap	C 489	21	0.9	728	13	US-10-027-632-140837	Sequence 140837,
417	21	0.9	547	13	US-10-027-632-47318	Sequence 47318, A	C 490	21	0.9	731	13	US-10-027-632-18111	Sequence 18111, A
C 418	21	0.9	549	13	US-10-027-632-254297	Sequence 254297,	C 491	21	0.9	731	13	US-10-027-632-151734	Sequence 151734,
C 419	21	0.9	549	13	US-10-027-632-254298	Sequence 254298,	492	21	0.9	737	13	US-10-027-632-18667	Sequence 18667, A
C 420	21	0.9	550	13	US-10-027-632-51289	Sequence 51289, A	493	21	0.9	750	13	US-10-027-632-3802	Sequence 3802, Ap
C 421	21	0.9	551	12	US-09-814-353-5694	Sequence 5694, Ap	494	21	0.9	750	13	US-10-027-632-3803	Sequence 3803, Ap
C 422	21	0.9	551	12	US-09-814-353-5694	Sequence 11978, A	495	21	0.9	750	13	US-10-027-632-3804	Sequence 3804, Ap
C 423	21	0.9	551	12	US-09-814-353-11978	Sequence 188340, A	496	21	0.9	752	13	US-10-027-632-11480	Sequence 11480, A
C 424	21	0.9	552	13	US-10-027-632-188340	Sequence 87425, A	C 497	21	0.9	757	9	US-09-770-445-978	Sequence 978, App
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ALIGNMENTS

RESULT 1
US-09-738-973-440
; Sequence 440, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 440
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-738-973-440

Query Match 100.0%; Score 2239; DB 10; Length 2239;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	361	ACTTTACTAGGGGAGTCTCCATTATCATTTGGCACCATTGGAGCAGGAATCTTCATC	420
Db	361	ACTTTACTAGGGGAGTCTCCATTATCATTTGGCACCATTGGAGCAGGAATCTTCATC	420
QY	421	TCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG	480
Db	421	TCTCCTAAGGGCGTGCTCCAGAACACGGGCAGCGTGGGCATGTCTCTGACCATCTGGACG	480
QY	481	GTGTGTGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATA	540
Db	481	GTGTGTGGGTCCTGTCACTATTTGGAGCTTTGTCTTATGCTGAATTTGGGAACAATA	540
QY	541	AAGAAATCTGGAGTCAATTACACATATATTTGGAGTCTTTGGTCCATTACCGCTTTT	600
Db	541	AAGAAATCTGGAGTCAATTACACATATATTTGGAGTCTTTGGTCCATTACCGCTTTT	600
QY	601	GTACGAGTCTGGTGGAACTCCTCATATAACGCCCTGCAGCTACTGCTGTGATATCCCTG	660
Db	601	GTACGAGTCTGGTGGAACTCCTCATATAACGCCCTGCAGCTACTGCTGTGATATCCCTG	660
QY	661	GCATTTGGACGCTACATTTCTGGAAACCATTTTATTTCAATGTGAAATCCCTGAACTGG	720
Db	661	GCATTTGGACGCTACATTTCTGGAAACCATTTTATTTCAATGTGAAATCCCTGAACTGG	720
QY	721	ATCAAGCTCATTTACGCTGTGGGCATAACTGTAGTCAATGCTTAAATAGCATGATGTC	780
Db	721	ATCAAGCTCATTTACGCTGTGGGCATAACTGTAGTCAATGCTTAAATAGCATGATGTC	780
QY	781	AGCTGGAGCGCCGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATCTTGATA	840
Db	781	AGCTGGAGCGCCGATCCAGATTTTCTTAACCTTTTGCAGCTCACAGCAATCTTGATA	840
QY	841	ATTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGCAGAACTTTAAAGACGCC	900
Db	841	ATTATAGTCCCTGGAGTTATGAGCTAATTAAGGTCAAACGCAGAACTTTAAAGACGCC	900
QY	901	TTTTTCAGGAAGAGATTCAAGTATTACCGGTTGCCACTGGCTTTTATTTATGGAATGAT	960
Db	901	TTTTTCAGGAAGAGATTCAAGTATTACCGGTTGCCACTGGCTTTTATTTATGGAATGAT	960
QY	961	GCATATGCTGGCTGGTTTACCTCAACTTTTACTGAAGAAGTAGAAAAACCCCTGAAAAA	1020
Db	961	GCATATGCTGGCTGGTTTACCTCAACTTTTACTGAAGAAGTAGAAAAACCCCTGAAAAA	1020
QY	1021	ACCATTCCCCTTGAATATGTATATCCATGGCATTGTACCATTGGCTATGTGCTGACA	1080
Db	1021	ACCATTCCCCTTGAATATGTATATCCATGGCATTGTACCATTGGCTATGTGCTGACA	1080

QY 1081 AATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTGCTTTCAAAATGCAGTGGCA 1140
Db |||||
1081 AATGTGGCCTACTTTACGACCATTAAATGCTGAGGAGCTGCTGCTTTCAAAATGCAGTGGCA 1140
QY 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATAGCAGTTCCGATCTTTGTGGCC 1200
Db |||||
1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATAGCAGTTCCGATCTTTGTGGCC 1200
QY 1201 CTCTCCTGCTTTTGGCTCCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATCTATGTT 1260
Db |||||
1201 CTCTCCTGCTTTTGGCTCCCATGAACGGTGGTGTGTTGCTGTCTCCAGGTTATCTATGTT 1260
QY 1261 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCGGCAAGCACACT 1320
Db |||||
1261 GCGTCTCGAGAGGGTCACCTTCCAGAAATCCTCTCCATGATTCATGTCGGCAAGCACACT 1320
QY 1321 CCTCTACCAGCTGTTATTGTTTTCACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGAC 1380
Db |||||
1321 CCTCTACCAGCTGTTATTGTTTTCACCCCTTTGACAAATGATAATGCTCTTCTCTGGAGAC 1380
QY 1381 CTCGACAGTCTTTTGAATTCCTCAGTTTTGCCAGTGGCTTTTATTGGCTGGCAGTT 1440
Db |||||
1381 CTCGACAGTCTTTTGAATTCCTCAGTTTTGCCAGTGGCTTTTATTGGCTGGCAGTT 1440
QY 1441 GCTGGGCTGATTTAATCTTCGATACAAAATGCCAGATATGTCCTTTTCAAGTGCCA 1500
Db |||||
1441 GCTGGGCTGATTTAATCTTCGATACAAAATGCCAGATATGTCCTTTTCAAGTGCCA 1500
QY 1501 CTGTTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGTTGCCCTTTCCCTCTAT 1560
Db |||||
1501 CTGTTTCATCCCAGCTTTGTTTTCCTTCACATGCCTCTTCATGTTGCCCTTTCCCTCTAT 1560
QY 1561 TCGGACCCCATTTAGTACAGGATTTGGCTTCGTCATCACTCTGACTGGAGTCCCTCGGTAT 1620
Db |||||
1561 TCGGACCCCATTTAGTACAGGATTTGGCTTCGTCATCACTCTGACTGGAGTCCCTCGGTAT 1620
QY 1621 TATCTCTTTATTATATGGGCAAGAAACCCAGGTGTTTGAATAATGTCAGAGAAAATA 1680
Db |||||
1621 TATCTCTTTATTATATGGGCAAGAAACCCAGGTGTTTGAATAATGTCAGAGAAAATA 1680
QY 1681 ACCAGAACATTACAAATATFACTGGAAGTTGTACCAGAGAAAGATAAGTTATGAACTAAT 1740
Db |||||
1681 ACCAGAACATTACAAATATFACTGGAAGTTGTACCAGAGAAAGATAAGTTATGAACTAAT 1740
QY 1741 GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTACTTCAT 1800
Db |||||
1741 GGACTTGAGATCTTGGCAATCTGCCCAAGGGGAGACACAAAATAGGGATTTTACTTCAT 1800
QY 1801 TTTCTGAAAGCTAGAGAAATTACAACTTTTGGTGATAAACAAGGAGTCAGTTATTTTA 1860
Db |||||
1801 TTTCTGAAAGCTAGAGAAATTACAACTTTTGGTGATAAACAAGGAGTCAGTTATTTTA 1860
QY 1861 TTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
Db |||||
1861 TTCATATATTTTAGCATATTCGAACTAATTTCTAAGAAATTTAGTTATAACTCTATGTAG 1920
QY 1921 TTATAGAAAGTGAATATGCACTTATTTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACC 1980
Db |||||
1921 TTATAGAAAGTGAATATGCACTTATTTCTATGAGTCGCACAATTTCTTGAGTCTCTGATACC 1980
QY 1981 TACCTATTGGGGTTAGGAGAAAAGACTAGACAATTTACTATGTGGTCATTTCTCTACAACAT 2040
Db |||||
1981 TACCTATTGGGGTTAGGAGAAAAGACTAGACAATTTACTATGTGGTCATTTCTCTACAACAT 2040
QY 2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTT 2100
Db |||||
2041 ATGTTAGCACGGCAAGAACCTTCAAATTTGAAGACTGAGATTTTCTGTATATATGGGTT 2100
QY 2101 TTGTAAAGATGGTTTTACACACTACAGATGTCTATACGTGAAAAGTGTTCATTTCTG 2160
Db |||||
2101 TTGTAAAGATGGTTTTACACACTACAGATGTCTATACGTGAAAAGTGTTCATTTCTG 2160
QY 2161 AAAAAAAGCATACATCATGATTATGGCAAGAGGAGAGAGGTAGAGCTGTTCTTAAATT 2220

Db 2161 AAAAAAAGCATACATCATGATTATGGCAAGAGGAGAGGTAGAGCTGTTCTTAAATT 2220
QY 2221 TATTAAAAAATAAAAAAAAAA 2239
Db |||||
2221 TATTAAAAAATAAAAAAAAAA 2239
RESULT 2
US-09-854-133-440
; Sequence 440, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 440
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-854-133-440
Query Match 100.0%; Score 2239; DB 10; Length 2239;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAGGTTGAAGTGACGACAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
Db |||||
1 GGAGGTTGAAGTGACGACAGATCATGCCAGCTGGGTGACAGTGAGACTCTGTCTCAAAC 60
QY 61 AGAATTAAGGAAAAAGAAAGAAAGAGAGAGGAAATTCAGGCCAATTGTGG 120
Db |||||
61 AGAATTAAGGAAAAAGAAAGAAAGAGAGAGGAAATTCAGGCCAATTGTGG 120
QY 121 CATAGATTTTATCATATTTCTGGATTTTGTGATTTTGTGATTTCTCATCTGGATTCA 180
Db |||||
121 CATAGATTTTATCATATTTCTGGATTTTGTGATTTTGTGATTTCTCATCTGGATTCA 180
QY 181 GGAAGCCCTGTGTGTCCACCATCTCCAAGAGAGTTTACCTGCAGGGAATGTTAACGGG 240
Db |||||
181 GGAAGCCCTGTGTGTCCACCATCTCCAAGAGAGTTTACCTGCAGGGAATGTTAACGGG 240
QY 241 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGAGCGCTTTTCAGGAAGAGAC 300
Db |||||
241 AGGCTGCCCTTCCCTGGGCAACAAGGAGCCACCTGGGAGGAGCGCTTTTCAGGAAGAGAC 300
QY 301 GCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGGAAAGTC 360
Db |||||
301 GCCTTTTCAGGAAGAGACGCCTTTTCAGGAAGAGAGAAAGTGCAGCTGAAGGAAAGTC 360
QY 361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATC 420
Db |||||
361 ACTTTACTGAGGGAGTCTCCATTATCATTTGGCACCATCATTTGGAGCAGGAATCTTCATC 420
QY 421 TCTCCTAAGGCGTCTCCAGAACACGGGAGCGTGGGCATGTCTCTGACCATCTGGACG 480
Db |||||
421 TCTCCTAAGGCGTCTCCAGAACACGGGAGCGTGGGCATGTCTCTGACCATCTGGACG 480
QY 481 GTGTGTGGGTCCTGTCACTATTGTGGAGCTTTGTCTTATGCTGAATTGGGAACAATA 540
Db |||||
481 GTGTGTGGGTCCTGTCACTATTGTGGAGCTTTGTCTTATGCTGAATTGGGAACAATA 540
QY 541 AAGAAATCTGGAGGTCATTACACATATATTTTGAAGTCTTTGGTCCATTACCAGCTTTT 600
Db |||||

Db 541 AAGAAATCTGAGGTCAATTACACATATATTTTGGAAAGTCTTTGGTCCATTACCAGCTTTT 600

Qy 601 GTACGAGTCTGGGTGGAACCTCCTCATATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660

Db 601 GTACGAGTCTGGGTGGAACCTCCTCATATACGCCCTGCAGCTACTGCTGTGATATCCCTG 660

Qy 661 GCATTGTGACGCTACATTCTGGAACCAATTTTATTCAATGTGAATCCCTGAACCTTGGC 720

Db 661 GCATTGTGACGCTACATTCTGGAACCAATTTTATTCAATGTGAATCCCTGAACCTTGGC 720

Qy 721 ATCAAGCTCAATACAGCTGTGGGCATAAAGTGTAGTGTCTCTAAATAGCATGAGTGC 780

Db 721 ATCAAGCTCAATACAGCTGTGGGCATAAAGTGTAGTGTCTCTAAATAGCATGAGTGC 780

Qy 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGGCAAGCTCACAGCAATTTCTGATA 840

Db 781 AGCTGGAGCGCCGGATCCAGATTTTCTTAACCTTTTGGCAAGCTCACAGCAATTTCTGATA 840

Qy 841 ATTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAACCGCAGAACTTTAAAGACGCC 900

Db 841 ATTATAGTCCCTGGAGTTATGCAGCTAATTAAGGTCAAACCGCAGAACTTTAAAGACGCC 900

Qy 901 TTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTAT 960

Db 901 TTTTCAGGAAGAGATTCAAGTATTACGCGGTTGCCACTGGCTTTTATTATGGAATGTAT 960

Qy 961 GCATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020

Db 961 GCATATGCTGGCTGGTTTACCTCAACTTTGTACTGAAGAAGTAGAAAAACCTGAAAAA 1020

Qy 1021 ACCATTCCCTTGCATATATATATCCATGGCCATTGTACCATTTGGCTATGTCTGACA 1080

Db 1021 ACCATTCCCTTGCATATATATATCCATGGCCATTGTACCATTTGGCTATGTCTGACA 1080

Qy 1081 AATGTGCGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAATGCAGTGGCA 1140

Db 1081 AATGTGCGCTACTTTACGACCAATTAATGCTGAGGAGCTGCTGCTTTCAATGCAGTGGCA 1140

Qy 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCGATCTTTTGTGCC 1200

Db 1141 GTGACCTTTTCTGAGCGGCTACTGGGAAATTTCTCATTTAGCAGTTCGATCTTTTGTGCC 1200

Qy 1201 CTCTCCTGCTTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGTCTCCAGGTTATTTCTATGTT 1260

Db 1201 CTCTCCTGCTTTTGGCTCCATGAACGGTGGTGTGTTTGTCTGTCTCCAGGTTATTTCTATGTT 1260

Qy 1261 GCGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATCATGTCGCGAAGCACACT 1320

Db 1261 GCGTCTCGAGAGGGTCACTTCCAGAAATCCTCTCCATGATCATGTCGCGAAGCACACT 1320

Qy 1321 CCTCTACAGCTGTTATTGTTTTGCACCCCTTTGACAAATGAATATGCTCTTCTCTGGAGAC 1380

Db 1321 CCTCTACAGCTGTTATTGTTTTGCACCCCTTTGACAAATGAATATGCTCTTCTCTGGAGAC 1380

Qy 1381 CTGACAGTCTTTTGAATTTCTCAGTTTGGCAGGTGGCTTTTATTGGGCTGGCAGTT 1440

Db 1381 CTGACAGTCTTTTGAATTTCTCAGTTTGGCAGGTGGCTTTTATTGGGCTGGCAGTT 1440

Qy 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTTCAAGGTGCCA 1500

Db 1441 GCTGGGCTGATTTATCTTCGATACAAATGCCAGATATGCATCGTCTTTTCAAGGTGCCA 1500

Qy 1501 CTGTTTCATCCAGCTTTGTTTTCTTCATATGCCTCTTCATGGTTGCCCTTTCCCTCTAT 1560

Db 1501 CTGTTTCATCCAGCTTTGTTTTCTTCATATGCCTCTTCATGGTTGCCCTTTCCCTCTAT 1560

Qy 1561 TCGGACCCATTTAGTACAGGATTTGGCTTCGTATCATCTCTGACTGGAGTCCCTGCGTAT 1620

Db 1561 TCGGACCCATTTAGTACAGGATTTGGCTTCGTATCATCTCTGACTGGAGTCCCTGCGTAT 1620

Qy 1621 TATCTCTTTATATATGGGACAGAAACCCAGGTGGTTTGAATAATGTTCAGAGAAATA 1680

Db 1621 TATCTCTTTATATATGGGACAGAAACCCAGGTGGTTTGAATAATGTTCAGAGAAATA 1680

RESULT 3

US-10-144-649A-440

; Sequence 440, Application US/10144649A

; Publication No. US20030118599A1

; GENERAL INFORMATION:

; APPLICANT: Lodes, Michael J.

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Algate, Paul A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.475C11

; CURRENT APPLICATION NUMBER: US/10/144,649A

; CURRENT FILING DATE: 2002-08-21

; NUMBER OF SEQ ID NOS: 749

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 440

; LENGTH: 2239

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-144-649A-440

Query Match 100.0%; Score 2239; DB 14; Length 2239;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGGTTGAAGTGACGAGATCATGCCAGCCTGGGTGACAGTGAGACTGTCTCAAAC 60

Db 1 GGAGGTTGAAGTGACGAGATCATGCCAGCCTGGGTGACAGTGAGACTGTCTCAAAC 60

[illegible][illegible]

Db	2221	TATTA	AAAAAAAAAAAAA	2239
RESULT 4				
US-09-738-973-441				
; Sequence 441, Application US/09738973				
; Patent No. US20020110563A1				
; GENERAL INFORMATION:				
; APPLICANT: Reed, Steven G.				
; APPLICANT: Henderson, Robert A.				
; APPLICANT: Lodes, Michael J.				
; APPLICANT: Fling, Steven P.				
; APPLICANT: Mohamath, Raodoh				
; APPLICANT: Algate, Paul A.				
; APPLICANT: Secrist, Heather				
; APPLICANT: Indirias, Carol Yoseph				
; APPLICANT: Benson, Darin R.				
; APPLICANT: Elliot, Mark				
; APPLICANT: Mannion, Jane				
; APPLICANT: Kalos, Michael D.				
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR				
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER				
; FILE REFERENCE: 210121.475C9				
; CURRENT APPLICATION NUMBER: US/09/738,973				
; CURRENT FILING DATE: 2000-12-14				
; NUMBER OF SEQ ID NOS: 587				
; SOFTWARE: FastSeq for Windows Version 3.0				
; SEQ ID NO 441				
; LENGTH: 5981				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
US-09-738-973-441				
Query Match 83.4%; Score 1867; DB 10; Length 5981;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	334	GAGAAAGTGAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC	393	
Db	278	GAGAAAGTGAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC	337	
Qy	394	ACCATCATTTGGAGCAGGAATCTTCATCTCTCTTAAGGCGTCTCTCCAGAACACACGGGACG	453	
Db	338	ACCATCATTTGGAGCAGGAATCTTCATCTCTCTTAAGGCGTCTCTCCAGAACACACGGGACG	397	
Qy	454	GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCTGTGTCACATTTTGGAGCTTTG	513	
Db	398	GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCTGTGTCACATTTTGGAGCTTTG	457	
Qy	514	TCCTATGCTGAATTGGGAACAACATAAAGAAATCTGGAGTCAATACACATATATTTTG	573	
Db	458	TCCTATGCTGAATTGGGAACAACATAAAGAAATCTGGAGTCAATACACATATATTTTG	517	
Qy	574	GAAGTCTTTGGTCCATTACCGCTTTTGTACGAGTCTGGTGGAACTCCTCATATAATACGC	633	
Db	518	GAAGTCTTTGGTCCATTACCGCTTTTGTACGAGTCTGGTGGAACTCCTCATATAATACGC	577	
Qy	634	CCTGCAGTACTGCTGTGATATCCCTGGCATTTGGACGTACATTTCTGGAACCAATTTT	693	
Db	578	CCTGCAGTACTGCTGTGATATCCCTGGCATTTGGACGTACATTTCTGGAACCAATTTT	637	
Qy	694	ATTCAATGTGAAATCCCTGAACTTCGGATCAAGCTCATACAGCTGTGGGCATAACTGTA	753	
Db	638	ATTCAATGTGAAATCCCTGAACTTCGGATCAAGCTCATACAGCTGTGGGCATAACTGTA	697	
Qy	754	GTGATGGTCCCTAAATAGCATGAGTGTGAGCGCCGGATCCAGATTTTCTTAACC	813	
Db	698	GTGATGGTCCCTAAATAGCATGAGTGTGAGCGCCGGATCCAGATTTTCTTAACC	757	
Qy	814	TTTTGCAAGCTCACAGCAATTCGATAATTATAGTCCCTGGAGTTATGCAGCTAATTA	873	
Db	758	TTTTGCAAGCTCACAGCAATTCGATAATTATAGTCCCTGGAGTTATGCAGCTAATTA	817	

Db 1898 TCGCACAATCTTGAGTCTCTGATACCTACCTATTGGGTTAGGAGAAAGACTAGACAA 1957
QY 2014 TTACTATGTGGTCATTCTCTACAACATATGTAGCAGCGCAAGAACCTTCAAATTGAAG 2073
Db 1958 TTACTATGTGGTCATTCTCTACAACATATGTAGCAGCGCAAGAACCTTCAAATTGAAG 2017
QY 2074 ACTGAGATTTTCTGTATATATGGGTTTTGTAAGATGGTTTTTACACACTACAGATGTCT 2133
Db 2018 ACTGAGATTTTCTGTATATATGGGTTTTGTAAGATGGTTTTTACACACTACAGATGTCT 2077
QY 2134 ATACTGTGAAAGTGTTTTCAATTCTGAAAAAGCATACATCATGATTATGGCAAAGAG 2193
Db 2078 ATACTGTGAAAGTGTTTTCAATTCTGAAAAAGCATACATCATGATTATGGCAAAGAG 2137
QY 2194 GAGAGAA 2200
Db 2138 GAGAGAA 2144

RESULT 5
US-09-854-133-441
; Sequence 441, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodch
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-854-133-441

Query Match 83.4%; Score 1867; DB 10; Length 5981;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 334 GAGAAAGTGCAGCTGAAGAGGAAAGTCATTACTGAGGGGAGTCTCCATTATCATTTGGC 393
Db 278 GAGAAAGTGCAGCTGAAGAGGAAAGTCATTACTGAGGGGAGTCTCCATTATCATTTGGC 337
QY 394 ACCATCATTTGAGCAGGAATCTTTCATCTCTAAGGCGTGTCTCCAGAACACGGGCAGC 453
Db 338 ACCATCATTTGAGCAGGAATCTTTCATCTCTAAGGCGTGTCTCCAGAACACGGGCAGC 397
QY 454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGGGGTCCCTGTCACTATTGGAGCTTTG 513
Db 398 GTGGGCATGTCTCTGACCATCTGGACGGTGTGGGGTCCCTGTCACTATTGGAGCTTTG 457
QY 514 TCTTATGCTGAATGGGAACAACATATAAGAAATCTGGAGGTCATTACACATATATTTTG 573
Db 458 TCTTATGCTGAATGGGAACAACATATAAGAAATCTGGAGGTCATTACACATATATTTTG 517
QY 574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACAGTCTGGGTGGAACTCCTCATAATACGC 633
Db 518 GAAGTCTTTGGTCCATTACCAGCTTTTGTACAGTCTGGGTGGAACTCCTCATAATACGC 577
QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCAATTTGGACGCTACATTTCTGGAACCATTTTT 693
Db 578 CCTGCAGCTACTGCTGTGATATCCCTGGCAATTTGGACGCTACATTTCTGGAACCATTTTT 637
QY 694 ATTCAATGTGAATCCCTGAACTTGCATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753

Db 638 ATTCATGTGAAATCCCTGAACTTGGGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 697
QY 754 GTGATGGTCCTAAATAGCATGATGATGATGAGCTGGAGCGCCGGATCCAGATTTTCTTAACC 813
Db 698 GTGATGGTCCTAAATAGCATGATGATGATGAGCTGGAGCGCCGGATCCAGATTTTCTTAACC 757
QY 814 TTTTGCAAAGCTCACAGCAATCTGATAAATTATAGTCCCTGGAGTTATGCAGCTAATTAA 873
Db 758 TTTTGCAAAGCTCACAGCAATCTGATAAATTATAGTCCCTGGAGTTATGCAGCTAATTAA 817
QY 874 GGTCAAACGCAGAACTTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACCGGGTTG 933
Db 818 GGTCAAACGCAGAACTTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACCGGGTTG 877
QY 934 CCACCTGGCTTTTATTTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 993
Db 878 CCACCTGGCTTTTATTTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 937
QY 994 ACTGAAGAAGTAGAAAAACCTGAAAAAACCATTTCCCTTGCATATGTATATCCATGGCC 1053
Db 938 ACTGAAGAAGTAGAAAAACCTGAAAAAACCATTTCCCTTGCATATGTATATCCATGGCC 997
QY 1054 ATTGTCACCATTTGGCTATGTCTGACAAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1113
Db 998 ATTGTCACCATTTGGCTATGTCTGACAAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1057
QY 1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTT 1173
Db 1058 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTT 1117
QY 1174 TCATTAGCAGTTCCGATCTTTTGTGGCCCTCTCCTGCTTGGTCCATGAACGGTGGTGTG 1233
Db 1118 TCATTAGCAGTTCCGATCTTTTGTGGCCCTCTCCTGCTTGGTCCATGAACGGTGGTGTG 1177
QY 1234 TTTGCTGTCTCCAGGTTATTTATGTTGGCTCTCGAGAGGGTCACTTCCAGAAATCCTC 1293
Db 1178 TTTGCTGTCTCCAGGTTATTTATGTTGGCTCTCGAGAGGGTCACTTCCAGAAATCCTC 1237
QY 1294 TCCATGATTCATGTCGCAAGCACACTCCTCTACCAGCTGTATTGTTTGCACCCCTTTG 1353
Db 1238 TCCATGATTCATGTCGCAAGCACACTCCTCTACCAGCTGTATTGTTTGCACCCCTTTG 1297
QY 1354 ACAATGATAATGCTCTCTCGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTGTGC 1413
Db 1298 ACAATGATAATGCTCTCTCGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTGTGC 1357
QY 1414 AGGTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1473
Db 1358 AGGTGGCTTTTATTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1417
QY 1474 GATATGCATCGTCCCTTTCAAGGTGCCACTGTTTCATCCCAGCTTTGTTTCTTCACATGC 1533
Db 1418 GATATGCATCGTCCCTTTCAAGGTGCCACTGTTTCATCCCAGCTTTGTTTCTTCACATGC 1477
QY 1534 CTCTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
Db 1478 CTCTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1537
QY 1594 ATCACTCTGACTGGAGTCCCTGGCTATTATCTCTTTATATATGGGACAAGAAACCCAGG 1653
Db 1538 ATCACTCTGACTGGAGTCCCTGGCTATTATCTCTTTTATATATGGGACAAGAAACCCAGG 1597
QY 1654 TGGTTTAGAATAATGTCAGAGAAAAATAACCAGAACATTAACAAATAACTGGAAGTTGTA 1713
Db 1598 TGGTTTAGAATAATGTCAGAGAAAAATAACCAGAACATTAACAAATAACTGGAAGTTGTA 1657
QY 1714 CCAGAAGAAGATAAGTTTATGAACTAATGGACTTGAGATCTTTGGCAATCTGCCCCAAGGGA 1773
Db 1658 CCAGAAGAAGATAAGTTTATGAACTAATGGACTTGAGATCTTTGGCAATCTGCCCCAAGGGA 1717
QY 1774 GACACAAAATAGGGATTTTACTTCACTTTCTGAAAGTCTAGAGAAATTACAACCTTTGGTG 1833
Db 1718 GACACAAAATAGGGATTTTACTTCACTTTTCTGAAAGTCTAGAGAAATTACAACCTTTGGTG 1777

QY 1834 ATAAACAAAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACTAATTCT 1893
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1778 ATAAACAAAGGAGTCAGTTATTTTATTCATATATTTTAGCATATTCGAACTAATTCT 1837
QY 1894 AAGAAATTTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTTCTATGAG 1953
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1838 AAGAAATTTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTTCTATGAG 1897
QY 1954 TCGCACAAATCTTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAAGACTAGACAA 2013
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1898 TCGCACAAATCTTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAAGACTAGACAA 1957
QY 2014 TTACTATGTGTCATTTCTTACAACATATGTTAGCACGGCAAGAACCTTCAAATTGAAG 2073
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1958 TTACTATGTGTCATTTCTTACAACATATGTTAGCACGGCAAGAACCTTCAAATTGAAG 2017
QY 2074 ACTGAGATTTTCTGTATATATGCGTTTTTGAAAGATGGTTTTTACACACTACAGATGTCT 2133
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2018 ACTGAGATTTTCTGTATATATGCGTTTTTGAAAGATGGTTTTTACACACTACAGATGTCT 2077
QY 2134 ATACTGTGAAAAGTGTTTTCAATTCTGAAAAAAGCATACATCATGATTTATGGCAAAGAG 2193
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2078 ATACTGTGAAAAGTGTTTTCAATTCTGAAAAAAGCATACATCATGATTTATGGCAAAGAG 2137
QY 2194 GAGAGAA 2200
Db ||||||||
2138 GAGAGAA 2144

RESULT 6
US-10-144-649A-441
; Sequence 441, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-649A-441

Query Match 83.4%; Score 1867; DB 14; Length 5981;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 334 GAGAAAGTCAGCTGAAGAGGAAAGTCACCTTACTGAGGGGAGTCTCCATTATCATTTGGC 393
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
278 GAGAAAGTCAGCTGAAGAGGAAAGTCACCTTACTGAGGGGAGTCTCCATTATCATTTGGC 337
QY 394 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTAAGGGCGTGTCTCCAGAACACGGGCAGC 453
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
338 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTAAGGGCGTGTCTCCAGAACACGGGCAGC 397
QY 454 GTGGGCATGTCTCTGACCATCTGGACCGTGTGTGGGGTCTGTGACATTTTGGAGCTTTG 513
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
398 GTGGGCATGTCTCTGACCATCTGGACCGTGTGTGGGGTCTGTGACATTTTGGAGCTTTG 457
QY 514 TCTTATGCTGAATTGGGAACAACCTATAAAGAAATCTGGAGTTCATTACACATATATTTG 573
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
458 TCTTATGCTGAATTGGGAACAACCTATAAAGAAATCTGGAGTTCATTACACATATATTTG 517

QY 574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGC 633
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
518 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAATACGC 577
QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAAACCATTTTTT 693
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
578 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAAACCATTTTTT 637
QY 694 ATTCAATGTGAAATCCCTGAACTTCCGATCAAGCTCATTTACAGCTGTGGGCATAACTGTA 753
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
638 ATTCAATGTGAAATCCCTGAACTTCCGATCAAGCTCATTTACAGCTGTGGGCATAACTGTA 697
QY 754 GTGATGGTCTCTAAATAGCATGATGTCTAGCTGGAGCGCCCGATCCAGATTTTCTTAACC 813
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
698 GTGATGGTCTCTAAATAGCATGATGTCTAGCTGGAGCGCCCGATCCAGATTTTCTTAACC 757
QY 814 TTTTGCAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA 873
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
758 TTTTGCAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTAAA 817
QY 874 GGTCAAACGCAGAACCTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
818 GGTCAAACGCAGAACCTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 877
QY 934 CCACTGGCTTTTATATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 993
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
878 CCACTGGCTTTTATATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 937
QY 994 ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC 1053
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
938 ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC 997
QY 1054 ATTGTCACCATTTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1113
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
998 ATTGTCACCATTTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCATTAATGCTGAG 1057
QY 1114 GAGCTGCTGCTTTCAAATGCAAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1173
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1058 GAGCTGCTGCTTTCAAATGCAAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1117
QY 1174 TCATTAGCAGTTCCGATCTTTTGTGCCCCCTCTCCCTGCTTTGGCTCCATGAACGGTGGTGTG 1233
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1118 TCATTAGCAGTTCCGATCTTTTGTGCCCCCTCTCCCTGCTTTGGCTCCATGAACGGTGGTGTG 1177
QY 1234 TTTGCTGTCTCCAGGTTATTTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1293
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1178 TTTGCTGTCTCCAGGTTATTTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1237
QY 1294 TCCATGATTTCATGTCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGACCCCTTTG 1353
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1238 TCCATGATTTCATGTCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGACCCCTTTG 1297
QY 1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTTGCC 1413
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1298 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTTGCC 1357
QY 1414 AGGTGGCTTTTATTTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1473
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1358 AGGTGGCTTTTATTTGGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1417
QY 1474 GATATGCATCGTCTCTTTCAAGGTGCCACTGTTCATCCAGCTTTGTTTCTCAGTTTGCATGC 1533
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1418 GATATGCATCGTCTCTTTCAAGGTGCCACTGTTCATCCAGCTTTGTTTCTCAGTTTGCATGC 1477
QY 1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCCGACCCCATTTTAGTACAGGGATTGGCTTCGTC 1593
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1478 CTCTTCATGGTTGCCCTTTCCCTCTATTCCGACCCCATTTTAGTACAGGGATTGGCTTCGTC 1537
QY 1594 ATCACTCTGACTGGAGTCCCTGCGTATTTATCTCTTTTATTATATGGACAAGAAACCCAGG 1653
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1538 ATCACTCTGACTGGAGTCCCTGCGTATTTATCTCTTTTATTATATGGACAAGAAACCCAGG 1597
QY 1654 TGGTTTAGAATAATGTCAGAGAAAAATAACCAGAACATTACAAATAATACTGGAAAGTTGTA 1713

,

Db	1598	TGGTTTAGAATAATGTCAGAGAAATAACCGAACAATTACAAATAATACTGGAAGTTGTA	1657
QY	1714	CCAGAAGAAGATAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA	1773
Db	1658	CCAGAAGAAGATAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA	1717
QY	1774	GACACAAAATAGGGAATTTTACTTCAATTTCTGAAAGTCTAGAGAATTACAACCTTTGGTG	1833
Db	1718	GACACAAAATAGGGAATTTTACTTCAATTTCTGAAAGTCTAGAGAATTACAACCTTTGGTG	1777
QY	1834	ATAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTCT	1893
Db	1778	ATAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTCT	1837
QY	1894	AAGAAATTTAGTTATAACTCTATGTATGTATAGTATAGAAAAGTGAATATGCAGTTATCTATGAG	1953
Db	1838	AAGAAATTTAGTTATAACTCTATGTATGTATAGAAAAGTGAATATGCAGTTATCTATGAG	1897
QY	1954	TCGCACAATTTTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAAGACTAGACAA	2013
Db	1898	TCGCACAATTTTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAAGACTAGACAA	1957
QY	2014	TTACTATGTGGTCATTTCTTACAACATATGTTAGCACGGCAAAAGACCTTCAAATTGAAG	2073
Db	1958	TTACTATGTGGTCATTTCTTACAACATATGTTAGCACGGCAAAAGACCTTCAAATTGAAG	2017
QY	2074	ACTGAGATTTTCTGTATATATATGGGTTTTGTAAAGATGGTTTTTACACACTACAGATGTCT	2133
Db	2018	ACTGAGATTTTCTGTATATATATGGGTTTTGTAAAGATGGTTTTTACACACTACAGATGTCT	2077
QY	2134	ATACTGTGAAAAGTGTTTTCAATTTCTGAAAAAAGCATACATCATGATTATGGCAAAGAG	2193
Db	2078	ATACTGTGAAAAGTGTTTTCAATTTCTGAAAAAAGCATACATCATGATTATGGCAAAGAG	2137
QY	2194	GAGAGAA 2200	
Db	2138	GAGAGAA 2144	
RESULT 7			
US-10-144-649A-740			
; Sequence 740, Application US/10144649A			
; Publication No. US20030118599A1			
; GENERAL INFORMATION:			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Fan, Liqun			
; APPLICANT: Algate, Paul A.			
; APPLICANT: McNeill, Patricia D.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR			
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.475C11			
; CURRENT APPLICATION NUMBER: US/10/144,649A			
; CURRENT FILING DATE: 2002-08-21			
; NUMBER OF SEQ ID NOS: 749			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 740			
; LENGTH: 6080			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-144-649A-740			
Query Match 83.4%; Score 1867; DB 14; Length 6080;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	334	GAGAAAGTCAGCTGAAGAGGAAAGTCATTTACTGAGGGAGTCTCCATTATCATTGGC	393
Db	372	GAGAAAGTCAGCTGAAGAGGAAAGTCATTTACTGAGGGAGTCTCCATTATCATTGGC	431
QY	394	ACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGTCCAGAACACGGGCAGC	453

Db	432	ACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGGCGTGCTCCAGAACACGGGCAGC	491
QY	454	GTGGGCATGTCTCTGACCATCTGACCGGTGTGTGGGGTCCCTGTCTACTATTTGGAGCTTTG	513
Db	492	GTGGGCATGTCTCTGACCATCTGACCGGTGTGTGGGGTCCCTGTCTACTATTTGGAGCTTTG	551
QY	514	TCCTATGCTGAATTTGGGAACAACATATAAGAAATCTGGAGGTCATTACACATATATTTTG	573
Db	552	TCCTATGCTGAATTTGGGAACAACATATAAGAAATCTGGAGGTCATTACACATATATTTTG	611
QY	574	GAACTCTTTGGTCCATTACCAAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATATAACGC	633
Db	612	GAACTCTTTGGTCCATTACCAAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATATAACGC	671
QY	634	CCTGAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCATTTTTT	693
Db	672	CCTGAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCATTTTTT	731
QY	694	ATTCAATGTGAAATCCCTGAACTTGCATCAAGCTCAAGCTCATTACAGCTGTGGGCATAACTGTA	753
Db	732	ATTCAATGTGAAATCCCTGAACTTGCATCAAGCTCAAGCTCATTACAGCTGTGGGCATAACTGTA	791
QY	754	GTGATGGTCTTAAATAGCATGAGTGTACAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC	813
Db	792	GTGATGGTCTTAAATAGCATGAGTGTACAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC	851
QY	814	TTTTGCAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATATAA	873
Db	852	TTTTGCAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATATAA	911
QY	874	GGTCAAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTACGCGTTG	933
Db	912	GGTCAAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTACGCGTTG	971
QY	934	CCACTGGCTTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT	993
Db	972	CCACTGGCTTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT	1031
QY	994	ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC	1053
Db	1032	ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC	1091
QY	1054	ATTGTCACCATTTGGCTATGTCTGACAAATGTGGCCCTACTTTACGACCATTAATGCTGAG	1113
Db	1092	ATTGTCACCATTTGGCTATGTCTGACAAATGTGGCCCTACTTTACGACCATTAATGCTGAG	1151
QY	1114	GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1173
Db	1152	GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1211
QY	1174	TCATTAGCAGTTCGGATCTTTTGTGCCCCTCTCTGCTTTGGCTCCATGAACGGTGGTGTG	1233
Db	1212	TCATTAGCAGTTCGGATCTTTTGTGCCCCTCTCTGCTTTGGCTCCATGAACGGTGGTGTG	1271
QY	1234	TTTGTGCTCTCCAGGTTATTTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC	1293
Db	1272	TTTGTGCTCTCCAGGTTATTTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC	1331
QY	1294	TCCATGATTCATGTCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGCACCCCTTG	1353
Db	1332	TCCATGATTCATGTCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGCACCCCTTG	1391
QY	1354	ACAATGATAATGCTCTTCTGTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTTGGC	1413
Db	1392	ACAATGATAATGCTCTTCTGTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTTGGC	1451
QY	1414	AGGTGGCTTTTTATTGGCTGGCAGTTGCTGGGTGATTTATCTTCGATACAAATGCCCA	1473
Db	1452	AGGTGGCTTTTTATTGGCTGGCAGTTGCTGGGTGATTTATCTTCGATACAAATGCCCA	1511
QY	1474	GATATGCATCGTCCCTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTTCTTCACATGC	1533
Db	1512	GATATGCATCGTCCCTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTTCTTCACATGC	1571

QY 1534 CTCTTCATGGTTGCCCTTCCCTCTATTCCGACCCATTTAGTACAGGATTTGGCTTCGTC 1593
Db |||||
QY 1572 CTCTTCATGGTTGCCCTTCCCTCTATTCCGACCCATTTAGTACAGGATTTGGCTTCGTC 1631
Db |||||
QY 1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTTATTATATGGGACAAGAAACCCAGG 1653
Db |||||
QY 1632 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTTATTATATGGGACAAGAAACCCAGG 1691
Db |||||
QY 1654 TGGTTTAGAATAATGTGAGAGAAATAAACAGAACATTACAAATAATACTGGAAGTTGTA 1713
Db |||||
QY 1692 TGGTTTAGAATAATGTGAGAGAAATAAACAGAACATTACAAATAATACTGGAAGTTGTA 1751
Db |||||
QY 1714 CCAGAAGAAGATAAGTTATGAACATAATGGACTTTGGCAATCTGCCCAAGGGGA 1773
Db |||||
QY 1752 CCAGAAGAAGATAAGTTATGAACATAATGGACTTTGGCAATCTGCCCAAGGGGA 1811
Db |||||
QY 1774 GACACAAAATAGGGATTTTACTTCAATTTCTGAAAGTCTAGAGAAATTACAACCTTTGGTG 1833
Db |||||
QY 1812 GACACAAAATAGGGATTTTACTTCAATTTCTGAAAGTCTAGAGAAATTACAACCTTTGGTG 1871
Db |||||
QY 1834 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACCTAATTTCT 1893
Db |||||
QY 1872 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACCTAATTTCT 1931
Db |||||
QY 1894 AAGAAATTTAGTTATTAACCTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTTCTATGAG 1953
Db |||||
QY 1932 AAGAAATTTAGTTATTAACCTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTTCTATGAG 1991
Db |||||
QY 1954 TCGCACAAATCTCTGAGTCTCTGATACCTTACCTATTTGGGGTTAGGAGAAAAGACTAGACAA 2013
Db |||||
QY 1992 TCGCACAAATCTCTGAGTCTCTGATACCTTACCTATTTGGGGTTAGGAGAAAAGACTAGACAA 2051
Db |||||
QY 2014 TTACTATGTGGTCAATCTCTACAACATATGTTAGACGGCAAGAACCTTCAAATTTGAAG 2073
Db |||||
QY 2052 TTACTATGTGGTCAATCTCTACAACATATGTTAGACGGCAAGAACCTTCAAATTTGAAG 2111
Db |||||
QY 2074 ACTGAGATTTTCTGTATATATAGGGTTTGTAAAGATGGTTTTTACACACTACAGATGTCT 2133
Db |||||
QY 2112 ACTGAGATTTTCTGTATATATAGGGTTTGTAAAGATGGTTTTTACACACTACAGATGTCT 2171
Db |||||
QY 2134 ATACTGTGAAAAGTGTCTTCAATCTGAAAAAAGCATACATCATGATTATGGCAAAGAG 2193
Db |||||
QY 2172 ATACTGTGAAAAGTGTCTTCAATCTGAAAAAAGCATACATCATGATTATGGCAAAGAG 2231
Db |||||
QY 2194 GAGAGAA 2200
Db |||||
QY 2232 GAGAGAA 2238
Db |||||

RESULT 8
US-10-163-866-31
; Sequence 31, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31

; LENGTH: 3144
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-31

Query Match 81.1%; Score 1816; DB 14; Length 3144;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1866; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GAGAAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTTGGC 393
Db |||||
QY 106 GAGAAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTTGGC 165
Db |||||
QY 394 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTAAGGGCGTGTCCAGAACACGGGCAGC 453
Db |||||
QY 166 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTAAGGGCGTGTCCAGAACACGGGCAGC 225
Db |||||
QY 454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCTACTATTTGGAGCTTTTG 513
Db |||||
QY 226 GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCTACTATTTGGAGCTTTTG 285
Db |||||
QY 514 TCTTATGCTCAATTTGGGAACAACATATAAGAAATCTGGAGGTCAATTACACATATATTTTG 573
Db |||||
QY 286 TCTTATGCTCAATTTGGGAACAACATATAAGAAATCTGGAGGTCAATTACACATATATTTTG 345
Db |||||
QY 574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCTCATAATACGC 633
Db |||||
QY 346 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCTCATAATACGC 405
Db |||||
QY 634 CCTGCAGCTACTGTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCATTTTTT 693
Db |||||
QY 406 CCTGCAGCTACTGTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCATTTTTT 465
Db |||||
QY 694 ATTCAATGTGAAATCCCTGAACCTTGGATCAAGCTCATTACAGTGTGGGCATAACTGTA 753
Db |||||
QY 466 ATTCAATGTGAAATCCCTGAACCTTGGATCAAGCTCATTACAGTGTGGGCATAACTGTA 525
Db |||||
QY 754 GTGATGGTCTTAAATAGCATGATGTGAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC 813
Db |||||
QY 526 GTGATGGTCTTAAATAGCATGATGTGAGCTGGAGCGCCCGGATCCAGATTTTCTTAACC 585
Db |||||
QY 814 TTTTGAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATATAA 873
Db |||||
QY 586 TTTTGAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATATAA 645
Db |||||
QY 874 GGTCAAACGCAGAACTTTTAAAGACGCTTTTTCAGGAAGAGATTAAGTATTACGGGTG 933
Db |||||
QY 646 GGTCAAACGCAGAACTTTTAAAGACGCTTTTTCAGGAAGAGATTAAGTATTACGGGTG 705
Db |||||
QY 934 CCCTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 993
Db |||||
QY 706 CCCTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTTACCTCAACTTTGTT 765
Db |||||
QY 994 ACTGAAGAAGTAGAAAACCCGTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC 1053
Db |||||
QY 766 ACTGAAGAAGTAGAAAACCCGTGAAAAAACCATTTCCCTTGCATAATGTATATCCATGGCC 825
Db |||||
QY 1054 ATTGTCAACCATTTGGCTATGTGTGACAAATGTGGCCCTACTTTACGACCATTAATGCTGAG 1113
Db |||||
QY 826 ATTGTCAACCATTTGGCTATGTGTGACAAATGTGGCCCTACTTTACGACCATTAATGCTGAG 885
Db |||||
QY 1114 GAGCTGCTGCTTTCAAATGAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1173
Db |||||
QY 886 GAGCTGCTGCTTTCAAATGAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 945
Db |||||
QY 1174 TCATTAGCAGTTCGGATCTTTGTTGCCCTCTCTCTGCTTTGGCTCCATGAACGGTGTGTG 1233
Db |||||
QY 946 TCATTAGCAGTTCGGATCTTTGTTGCCCTCTCTCTGCTTTGGCTCCATGAACGGTGTGTG 1005
Db |||||
QY 1234 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1293
Db |||||
QY 1006 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1065
Db |||||

QY 1294 TCCATGATTCATGTCCGCAAGCACACCTCTACCAGCTGTTATTGTTTGCACCCCTTTG 1353
|||||
Db 1066 TCCATGATTCATGTCCGCAAGCACACCTCTACCAGCTGTTATTGTTTGCACCCCTTTG 1125
QY 1354 ACAATGATAAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTCCTCAGTTTGGC 1413
|||||
Db 1126 ACAATGATAAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTCCTCAGTTTGGC 1185
QY 1414 AGGTGGCTTTTATATGGCTGGCAGTTGCTGGCTGATTTATCTCGATACAAATGCCCA 1473
|||||
Db 1186 AGGTGGCTTTTATATGGCTGGCAGTTGCTGGCTGATTTATCTCGATACAAATGCCCA 1245
QY 1474 GATAATGATCGTCCCTTTCAAGGTGCCACTGTTCAATCCAGCTTTGTTTCTTCCATGTC 1533
|||||
Db 1246 GATAATGATCGTCCCTTTCAAGGTGCCACTGTTCAATCCAGCTTTGTTTCTTCCATGTC 1305
QY 1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGATTGGCTTCGTC 1593
|||||
Db 1306 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGATTGGCTTCGTC 1365
QY 1594 ATCACTCTGACTGGAGTCCCTCGGTATATCTCTTTATATATGGGACAAGAAACCCAGG 1653
|||||
Db 1366 ATCACTCTGACTGGAGTCCCTCGGTATATCTCTTTATATATGGGACAAGAAACCCAGG 1425
QY 1654 TGGTTTAGAATAATGTCAGAGAAAATAACAGAACATTACAAATAATACTGGAAGTTGTA 1713
|||||
Db 1426 TGGTTTAGAATAATGTCAGAGAAAATAACAGAACATTACAAATAATACTGGAAGTTGTA 1485
QY 1714 CCAGAAGAGATAAGTTATGAACATAATGACTTGAGATCTTGGCAATCTGCCAAGGGGA 1773
|||||
Db 1486 CCAGAAGAGATAAGTTATGAACATAATGACTTGAGATCTTGGCAATCTGCCAAGGGGA 1545
QY 1774 GACACAAAATAGGGATTTTACTTTCATTTTCTGAAAGTCTAGAGAATTACAACCTTTGGTG 1833
Db 1546 GACACAAAATAGGGATTTTACTTTCATTTTCTGAAAGTCTAGAGAATTACAACCTTTGGTG 1605
QY 1834 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTTCT 1893
Db 1606 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTTCT 1665
QY 1894 AAGAAATTTAGTTATAACTCTATGAGTTATAGAAAGTGAATATGCAGTTATCTATGAG 1953
|||||
Db 1666 AAGAAATTTAGTTATAACTCTATGAGTTATAGAAAGTGAATATGCAGTTATCTATGAG 1725
QY 1954 TCGCACAAATCTTGAGTCTCTGATACCTACCTATTGGGTTAGAGAAAAGACTAGACAA 2013
|||||
Db 1726 TCGCACAAATCTTGAGTCTCTGATACCTACCTATTGGGTTAGAGAAAAGACTAGACAA 1785
QY 2014 TTACTATGTGGTCATTTCTACAAACATATGTTAGCACGGCAAGAACCTTCAAAATTGAAG 2073
|||||
Db 1786 TTACTATGTGGTCATTTCTACAAACATATGTTAGCACGGCAAGAACCTTCAAAATTGAAG 1845
QY 2074 ACTGAGATTTTCTGTATATATGGGTTTGTAAAGATGGTTTTTACACACTACAGATGCT 2133
|||||
Db 1846 ACTGAGATTTTCTGTATATATGGGTTTGTAAAGATGGTTTTTACACACTACAGATGCT 1905
QY 2134 ATACTGTGAAAAGTGTTTTCAAATTCGAAAAAAGCATACATCATGATTATGGCAAAGAG 2193
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Db 1906 ATACTGTGAAAAGTGTTTTCAAATTCGAAAAAAGCATACATCATGATTATGGCAAAGAG 1965
QY 2194 GAGAGAA 2200
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Db 1966 GAGAGAA 1972

RESULT 9
US-10-163-866-29
; Sequence 29, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C

; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-29

Query Match 76.9%; Score 1722; DB 14; Length 2482;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1772; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GAGAAAGTGCAGCTGAAGAGGAAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC 393
|||||
Db 337 GAGAAAGTGCAGCTGAAGAGGAAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGGC 396
QY 394 ACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGCGTGTCCAGAACACGGGCAGC 453
|||||
Db 397 ACCATCATTTGGAGCAGGAATCTTCATCTCTCCTAAGGCGTGTCCAGAACACGGGCAGC 456
QY 454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTGGAGCTTTG 513
|||||
Db 457 GTGGGCATGTCTCTGACCATCTGGACGGTATGTGGGTCCTGTCACTATTTGGAGCTTTG 516
QY 514 TCTTATGCTGAATTTGGAAACAACATAAAGAAATCTGGAGGTCAATTACACATATATTTTG 573
Db 517 TCTTATGCTGAATTTGGAAACAACATAAAGAAATCTGGAGGTCAATTACACATATATTTTG 576
QY 574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGTGGAACTCCTCATATACAGC 633
Db 577 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGTGGAACTCCTCATATATACGC 636
QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGTACATTCTTGGAAACCATTTTT 693
Db 637 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGTACATTCTTGGAAACCATTTTT 696
QY 694 ATTCAATGTGAAATCCCTGAACATTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
Db 697 ATTCAATGTGAAATCCCTGAACATTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 756
QY 754 GTGATGGTCCTAAATAGCATGAGTGTGAGCTGGAGCCCGGATCCAGATTTTCTTAACC 813
Db 757 GTGATGGTCCTAAATAGCATGAGTGTGAGCTGGAGCCCGGATCCAGATTTTCTTAACC 816
QY 814 TTTTGCAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATFAAA 873
Db 817 TTTTGCAAGCTCACAGCAATTTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATFAAA 876
QY 874 GGTCAAAACGCAGAACTTTTAAAGACGCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
Db 877 GGTCAAAACGCAGAACTTTTAAAGACGCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 936
QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGTGGCTGGTTTTTACCCTCAACTTTGTT 993
Db 937 CCACTGGCTTTTATTATGGAATGTATGCATATGTGGCTGGTTTTTACCCTCAACTTTGTT 996
QY 994 ACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTCCTTGCATATGTCAATATGTATATCATGGCC 1053
Db 997 ACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTCCTTGCATATGTCAATATGTATATCATGGCC 1056
QY 1054 ATTGTCACCATTTGGCTATGTGCTGACAAATGTGGCTACTTTACGACCATTATATGCTGAG 1113

Db	1057	ATTGTCACCATGGCTATGTGCTGACAAATGTGGCCCTACTTTACGACCAATTAATGCTGAG	1116
QY	1114	GAGCTGCTGCTTTCAAATGAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1173
Db	1117	GAGCTGCTGCTTTCAAATGAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1176
QY	1174	TCATTAGCAGTTCGGATCTTTGTTGCCCTCTCCCTGTTTGGCTCCATGAACGGTGGTGTG	1233
Db	1177	TCATTAGCAGTTCGGATCTTTGTTGCCCTCTCCCTGTTTGGCTCCATGAACGGTGGTGTG	1236
QY	1234	TTTGCTGTCTCCAGGTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCCGAAATCCTC	1293
Db	1237	TTTGCTGTCTCCAGGTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCCGAAATCCTC	1296
QY	1294	TCCATGATTCAATGTCGCGAAGCACACTCCTCTACAGCTGTTATTGTTTGCACCCCTTG	1353
Db	1297	TCCATGATTCAATGTCGCGAAGCACACTCCTCTACAGCTGTTATTGTTTGCACCCCTTG	1356
QY	1354	ACAAATGATAANGCTCTTCTCTGGAGACCTCGACAGCTCTTTTGAATTTCCCTCAGTTTGCC	1413
Db	1357	ACAAATGATAANGCTCTTCTCTGGAGACCTCGACAGCTCTTTTGAATTTCCCTCAGTTTGCC	1416
QY	1414	AGGTGGCTTTTATTGGCTGGCAGTTGCTGGGTGATTATCTTCGATACAAATGCCCA	1473
Db	1417	AGGTGGCTTTTATTGGCTGGCAGTTGCTGGGTGATTATCTTCGATACAAATGCCCA	1476
QY	1474	GATATGCATCGTCCCTTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTTCCTTCACATGC	1533
Db	1477	GATATGCATCGTCCCTTTCAAGGTGCCACTGTTTCATCCAGCTTTGTTTTCCTTCACATGC	1536
QY	1534	CTCTTTCATGGTTGCCCTTTCCCTCTATTTCGACCCCATTTAGTACAGGGATTGGCTTCGTC	1593
Db	1537	CTCTTTCATGGTTGCCCTTTCCCTCTATTTCGACCCCATTTAGTACAGGGATTGGCTTCGTC	1596
QY	1594	ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGCGACAAGAAACCCAGG	1653
Db	1597	ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGCGACAAGAAACCCAGG	1656
QY	1654	TGGTTTAGAATAATGTCAGAGAAAATAACAGAACATTACAAATAATCTGGAAGTTGTA	1713
Db	1657	TGGTTTAGAATAATGTCAGAGAAAATAACAGAACATTACAAATAATCTGGAAGTTGTA	1716
QY	1714	CCAGAAGAAGATAAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA	1773
Db	1717	CCAGAAGAAGATAAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA	1776
QY	1774	GACACAAAATAGGATTTTACTTTCATTTTCTGAAAGTCTAGAGAATTACAACTTTGGTG	1833
Db	1777	GACACAAAATAGGATTTTACTTTCATTTCTGAAAGTCTAGAGAATTACAACTTTGGTG	1836
QY	1834	ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACTAATTTCT	1893
Db	1837	ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACTAATTTCT	1896
QY	1894	AAGAAATTTTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCATGAG	1953
Db	1897	AAGAAATTTTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCATGAG	1956
QY	1954	TCGCACAATTCCTGAGTCTCTGATACCTACCTATTTGGGTTAGGAGAAAAGACTAGACAA	2013
Db	1957	TCGCACAATTCCTGAGTCTCTGATACCTATTTGGGTTAGGAGAAAAGACTAGACAA	2016
QY	2014	TTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAAGAACCTTCAAATTGAAG	2073
Db	2017	TTACTATGTGGTCATTCTCTACAACATATGTTAGCACGGCAAGAACCTTCAAATTGAAG	2076
QY	2074	ACTGAGATTTTCTGTATATATGCGTTTTGTAA	2106
Db	2077	ACTGAGATTTTCTGTATATATGCGTTTTGTAA	2109

US-10-133-013-40	
; Sequence 40, Application US/10133013	
; Publication No. US20030166903A1	
; GENERAL INFORMATION:	
; APPLICANT: Astromoff, Anna	
; APPLICANT: Bandman, Olga	
; APPLICANT: Cocks, Benjamin G.	
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE	
; FILE REFERENCE: PA-0049 US	
; CURRENT APPLICATION NUMBER: US/10/133,013	
; CURRENT FILING DATE: 2002-04-25	
; PRIOR APPLICATION NUMBER: 60/287,067	
; PRIOR FILING DATE: 2001-04-27	
; NUMBER OF SEQ ID NOS: 271	
; SOFTWARE: PERL Program	
; SEQ ID NO 40	
; LENGTH: 2041	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; NAME/KEY: misc feature	
; OTHER INFORMATION: Incyte ID No. US20030166903A1 406992.1	
; FEATURE:	
; NAME/KEY: unsure	
; LOCATION: 1923, 1998, 2026	
; OTHER INFORMATION: a, t, c, g, or other	
US-10-133-013-40	

Query Match		71.5%;	Score 1600;	DB 12;	Length 2041;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 1650;		Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	334	GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGC	393		
Db	347	GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGC	406		
QY	394	ACCATATTGGAGCAGGAATCTTCAATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGC	453		
Db	407	ACCATATTGGAGCAGGAATCTTCAATCTCTCTAAGGGCGTGCTCCAGAACACGGGCAGC	466		
QY	454	GTGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCTCACTATTTGGAGCTTTG	513		
Db	467	GTGGCATGTCTCTGACCATCTGGACGGTGTGTGGGGTCTGTCTCACTATTTGGAGCTTTG	526		
QY	514	TCATTATGCTGAATTGGGAACAACATATAAGAAATCTGGAGGTCAATTACACATATATTTTG	573		
Db	527	TCATTATGCTGAATTGGGAACAACATATAAGAAATCTGGAGGTCAATTACACATATATTTTG	586		
QY	574	GAACTCTTTGGTCCATTACCAAGCTTTTGTACGAGTCTGGTGGAACTCCTCATATAACGC	633		
Db	587	GAACTCTTTGGTCCATTACCAAGCTTTTGTACGAGTCTGGTGGAACTCCTCATATAACGC	646		
QY	634	CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTCTGGAAACCATTTT	693		
Db	647	CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTCTGGAAACCATTTT	706		
QY	694	ATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTCAATTACAGCTGTGGGCATAACTGTA	753		
Db	707	ATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTCAATTACAGCTGTGGGCATAACTGTA	766		
QY	754	GTGATGGTCTTAAATAGCATGAGTGTGAGTGGAGGCCCGGATCCAGATTTTCTTAACC	813		
Db	767	GTGATGGTCTTAAATAGCATGAGTGTGAGTGGAGGCCCGGATCCAGATTTTCTTAACC	826		
QY	814	TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTTAA	873		
Db	827	TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTTAA	886		
QY	874	GGTCAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTACGGGTTG	933		
Db	887	GGTCAAACGCAGAACTTTAAAGACGCCCTTTTCAGGAAGAGATTCAAGTATTACGGGTTG	946		
QY	934	CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTGTT	993		

Db	947	CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTGTT	1006
QY	994	ACTGAAGAAGTAGAAAACCCCTGAAAAACCATTCCCCTTGCATATGTATATCCATGGCC	1053
Db	1007	ACTGAAGAAGTAGAAAACCCCTGAAAAACCATTCCCCTTGCATATGTATATCCATGGCC	1066
QY	1054	ATTGTACCAATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCAATTAATGCTGAG	1113
Db	1067	ATTGTACCAATTGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCAATTAATGCTGAG	1126
QY	1114	GAGTGTCTCTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1173
Db	1127	GAGTGTCTCTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1186
QY	1174	TCATTAGCAGTCCGATCTTTGTGGCCTCTCCTGCTTTGGCTCCATGAACGGTGTGTG	1233
Db	1187	TCATTAGCAGTCCGATCTTTGTGGCCTCTCCTGCTTTGGCTCCATGAACGGTGTGTG	1246
QY	1234	TTTGTCTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC	1293
Db	1247	TTTGTCTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACCTTCCAGAAATCCTC	1306
QY	1294	TCCATGATTCAATGTCGCAAGCACACTCCCTCTACCAGCTGTTATTGTTTTCACCCCTTG	1353
Db	1307	TCCATGATTCAATGTCGCAAGCACACTCCCTCTACCAGCTGTTATTGTTTTCACCCCTTG	1366
QY	1354	ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTGCC	1413
Db	1367	ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTTCTCAGTTTTGCC	1426
QY	1414	AGTGGCTTTTATTGGGCTGGCAGTTGCTGGCTGANTTATCTTCGATACAAAATGCCA	1473
Db	1427	AGTGGCTTTTATTGGGCTGGCAGTTGCTGGCTGANTTATCTTCGATACAAAATGCCA	1486
QY	1474	GATATGCATCGTCCCTTCAAGGTGCCACTGTTTCATCCCAGCTTGTGTTTCCCTTCACATGC	1533
Db	1487	GATATGCATCGTCCCTTCAAGGTGCCACTGTTTCATCCCAGCTTGTGTTTCCCTTCACATGC	1546
QY	1534	CTCTTCATGGTTGCCCTTCCCTCTATTCGGACCCATTTTAGTACAGGGATTGGCTTCGTC	1593
Db	1547	CTCTTCATGGTTGCCCTTCCCTCTATTCGGACCCATTTTAGTACAGGGATTGGCTTCGTC	1606
QY	1594	ATCACTCTGACTGGAGTCCCTCGGTATTATCTCTTTATTATATGGGACAAGAAACCCAGG	1653
Db	1607	ATCACTCTGACTGGAGTCCCTCGGTATTATCTCTTTATTATATGGGACAAGAAACCCAGG	1666
QY	1654	TGGTTTAGAATAATGTCAGAGAAAATAACCAAGAACATTACAAATAATACTGGAAGTTGTA	1713
Db	1667	TGGTTTAGAATAATGTCAGAGAAAATAACCAAGAACATTACAAATAATACTGGAAGTTGTA	1726
QY	1714	CCAGAGAAGATAAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGA	1773
Db	1727	CCAGAGAAGATAAGTTATGAACATAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGA	1786
QY	1774	GACACAAAATAGGGATTTTACTTCAATTTTCTGAAAGTCTAGAGAAATTACAACTTTGGTG	1833
Db	1787	GACACAAAATAGGGATTTTACTTCATTTTCTGAAAGTCTAGAGAAATTACAACTTTGGTG	1846
QY	1834	ATAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTTCT	1893
Db	1847	ATAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACATAATTTCT	1906
QY	1894	AAGAAATTAGTTATAACTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCATGAG	1953
Db	1907	AAGAAATTAGTTATANCTCTATGTAGTTATAGAAAGTGAATATGCAGTTATTCATGAG	1966
QY	1954	TCGCACAATCTTGTAGTCTCTGTATACCTACC	1984
Db	1967	TCGCACAATCTTGTAGTCTCTGTATACCTACC	1997

US-10-247-671-78
; Sequence 78, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 78
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 406992.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1923, 1998, 2026
; OTHER INFORMATION: a, t, c, g, or other
US-10-247-671-78

Query Match	71.5%;	Score 1600;	DB 12;	Length 2041;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1650;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	334	GAGAAAGTGCAGCTGAAGAGGAAAGTCACITTTACTGAGGGGAGTCTCCATTATCATTTGGC	393	
Db	347	GAGAAAGTGCAGCTGAAGAGGAAAGTCACITTTACTGAGGGGAGTCTCCATTATCATTTGGC	406	
QY	394	ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTTAAGGGCGTGCTCCAGAACACGGGCAGC	453	
Db	407	ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTTAAGGGCGTGCTCCAGAACACGGGCAGC	466	
QY	454	GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTGGAGCTTTG	513	
Db	467	GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTGGAGCTTTG	526	
QY	514	TCTTATGCTGAATTGGGAACAACTATAAGAAATCTGGAGGTCAATACACATATATTTTG	573	
Db	527	TCTTATGCTGAATTGGGAACAACTATAAGAAATCTGGAGGTCAATACACATATATTTTG	586	
QY	574	GAAGTCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACTCCTCAATAACGC	633	
Db	587	GAAGTCTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACTCCTCAATAACGC	646	
QY	634	CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCATTTTTT	693	
Db	647	CCTGCAGCTACTGCTGTGATATCCCTGGCATTTTGGACGCTACATTTCTGGAACCATTTTTT	706	
QY	694	ATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTCATTAACAGCTGTGGGCATAACTGTA	753	
Db	707	ATTCAATGTGAAATCCCTGAACTTGGCATCAAGCTCATTAACAGCTGTGGGCATAACTGTA	766	
QY	754	GTGATGGTCCATAATAGCATGAGTGTCACTGGAGCGCCCGGATCCAGATTTCTTAACC	813	
Db	767	GTGATGGTCCATAATAGCATGAGTGTCACTGGAGCGCCCGGATCCAGATTTCTTAACC	826	
QY	814	TTTGTCAAGCTCACAGCAATCTGTATAATTATAGTCCCTGGAGTTATGCAGCTAATAAAA	873	
Db	827	TTTGTCAAGCTCACAGCAATCTGTATAATTATAGTCCCTGGAGTTATGCAGCTAATAAAA	886	
QY	874	GGTCAAACGCAGAACTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACGGGTTG	933	
Db	887	GGTCAAACGCAGAACTTTAAAGACGCCTTTTTCAGGAAGAGATTCAAGTATTACGGGTTG	946	

QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACTCAACTTTGTT 993
Db |||||
QY 947 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACTCAACTTTGTT 1006
Db |||||
QY 994 ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCAATCCCTTGCAATATGATATCCATGGCC 1053
Db |||||
QY 1007 ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCAATCCCTTGCAATATGATATCCATGGCC 1066
Db |||||
QY 1054 ATTGTCACCAATTGGCTATGTGCTGACAAATGCGCCTACTTTACGACCAATTAATGCTGAG 1113
Db |||||
QY 1067 ATTGTCACCAATTGGCTATGTGCTGACAAATGCGCCTACTTTACGACCAATTAATGCTGAG 1126
Db |||||
QY 1114 GAGCTGCTGCTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1173
Db |||||
QY 1127 GAGCTGCTGCTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1186
Db |||||
QY 1174 TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1233
Db |||||
QY 1187 TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1246
Db |||||
QY 1234 TTTGCTGTCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCAGAAATCCTC 1293
Db |||||
QY 1247 TTTGCTGTCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCAGAAATCCTC 1306
Db |||||
QY 1294 TCCATGATTCATGTCGCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGCACCCTTTG 1353
Db |||||
QY 1307 TCCATGATTCATGTCGCGCAAGCACACTCCTCTACAGCTGTTATTGTTTTGCACCCTTTG 1366
Db |||||
QY 1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTCCTCAGTTTGCC 1413
Db |||||
QY 1367 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAATTCCTCAGTTTGCC 1426
Db |||||
QY 1414 AGGTGGCTTTTATTGGGCTGGCAGTGGCTGGCTGATTTATCTTCGATACAAATGCCA 1473
Db |||||
QY 1427 AGGTGGCTTTTATTGGGCTGGCAGTGGCTGGCTGATTTATCTTCGATACAAATGCCA 1486
Db |||||
QY 1474 GATATGATCGTCCTTTCAAGGTGCCACTGTTCAATCCAGCTTTGTTTTCTTCACATGC 1533
Db |||||
QY 1487 GATATGATCGTCCTTTCAAGGTGCCACTGTTCAATCCAGCTTTGTTTTCTTCACATGC 1546
Db |||||
QY 1534 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1593
Db |||||
QY 1547 CTCTTCATGGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGGATTGGCTTCGTC 1606
Db |||||
QY 1594 ATCACTCTGACTGGAGTCCCTGCGTATATCTCTTTATTATATGGACAAGAAACCCAGG 1653
Db |||||
QY 1607 ATCACTCTGACTGGAGTCCCTGCGTATATCTCTTTATTATATGGACAAGAAACCCAGG 1666
Db |||||
QY 1654 TGGTTTAGAATAATGTCAGAGAAAAATAACCAAGACATTACAAATAATACCTGGAAGTTGTA 1713
Db |||||
QY 1667 TGGTTTAGAATAATGTCAGAGAAAAATAACCAAGACATTACAAATAATACCTGGAAGTTGTA 1726
Db |||||
QY 1714 CCAGAGAAGATAAGTTATGAACCTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA 1773
Db |||||
QY 1727 CCAGAGAAGATAAGTTATGAACCTAATGGACTTGAGATCTTGGCAATCTGCCCAAGGGGA 1786
Db |||||
QY 1774 GACAAAAATAGGGATTTTACTTCATTTTCTGAAAAGTCTAGAGAAATTACAACCTTTGGTG 1833
Db |||||
QY 1787 GACAAAAATAGGGATTTTACTTCATTTTCTGAAAAGTCTAGAGAAATTACAACCTTTGGTG 1846
Db |||||
QY 1834 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACCTAATTTCT 1893
Db |||||
QY 1847 ATAAACAAAAGGAGTCAGTTATTTTATTTCATATATTTTAGCATATTCGAACCTAATTTCT 1906
Db |||||
QY 1894 AAGAAATTTAGTTATAACTCTATGTAGTTATAGAAAAGTGAATATGCAGTTATTCATGAG 1953
Db |||||
QY 1907 AAGAAATTTAGTTATANCTCTATGTAGTTATAGAAAAGTGAATATGCAGTTATTCATGAG 1966
Db |||||
QY 1954 TCGCACAAATCTTTGAGTCTCTGATACCTACC 1984
Db |||||
QY 1967 TCGCACAAATCTTTGAGTCTCTGATACCTACC 1997
Db |||||

RESULT 12
US-10-163-866-30
; Sequence 30, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-30

Query Match 64.9%; Score 1454; DB 14; Length 1861;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTTGGC 393
Db |||||
QY 341 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGGAGTCTCCATTATCATTTGGC 400
Db |||||
QY 394 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTAAGGGCGTGTCCAGAACACGGGCAGC 453
Db |||||
QY 401 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTAAGGGCGTGTCCAGAACACGGGCAGC 460
Db |||||
QY 454 GTGGGCATGTCCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTGGAGCTTTG 513
Db |||||
QY 461 GTGGGCATGTCCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTGGAGCTTTG 520
Db |||||
QY 514 TCTTATGCTGAATTTGGGAACAACACTATAAGAAATCTGGAGGTCAATTACACATATATTTG 573
Db |||||
QY 521 TCTTATGCTGAATTTGGGAACAACACTATAAGAAATCTGGAGGTCAATTACACATATATTTG 580
Db |||||
QY 574 GAAAGTCTTTGGTCCATTACCAGCTTTTGTACAGGTCCTGGGTGGAACCTCCTCATAAATACGC 633
Db |||||
QY 581 GAAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACCTCCTCATAAATACGC 640
Db |||||
QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCAATTTGACCGCTACATTCTGGAACCACTTTT 693
Db |||||
QY 641 CCTGCAGCTACTGCTGTGATATCCCTGGCAATTTGACCGCTACATTCTGGAACCACTTTT 700
Db |||||
QY 694 ATTCAATGTGAAATCCCTGAACTTGGGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 753
Db |||||
QY 701 ATTCAATGTGAAATCCCTGAACTTGGGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 760
Db |||||
QY 754 GTGATGGTCCTAAATAGCATGAGTGTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 813
Db |||||
QY 761 GTGATGGTCCTAAATAGCATGAGTGTGCGATCAAGCTCATTACAGCTGTGGGCATAACTGTA 820
Db |||||
QY 814 TTTTGAAGCTCACAGCAATTTCTGATAATATAGTCCCTGGAGTTATGACAGCTAATAA 873
Db |||||
QY 821 TTTTGAAGCTCACAGCAATTTCTGATAATATAGTCCCTGGAGTTATGACAGCTAATAA 880
Db |||||
QY 874 GGTCAAACGCAGAACTTTAAAGACGCGCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
Db |||||
QY 881 GGTCAAACGCAGAACTTTAAAGACGCGCTTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 940
Db |||||
QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACTCAACTTTGTT 993
Db |||||

Db941

CCACTGGCTTTTATTATGGAATGATGATATGCTGGCTGGTTTACCTCAACTTTGTT

1000

Qy994

ACTGAAGAGTAGAAAACCCCTGAAAAACCAATCCCTTGCAATATGTATATCCATGGCC

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Db1001

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Qy1054

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Db1061

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Db1181

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Qy1234

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1293

Db1241

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1300

Qy1294

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1353

Db1301

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1360

Qy1354

ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAAATTCCTCAGTTTGGC

1413

Db1361

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Qy1414

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1473

Db1421

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1480

Qy1474

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Qy1654

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Db1661

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Qy1714

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1773

Db1721

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1780

Qy1774

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1833

Db1781

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1840

Qy1834

ATAAA 1838

Db1841

ATAAA 1845

Qy334

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393

Db114

GAGAAAGTGCAGCTGAAGAGGAAAGTCACCTTTACTGAGGGAGTCTCCATTATCATTTGC

173

Qy394

ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTAAGGGCGTCTCCAGAACACGGGCAGC

453

Db174

ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTAAGGGCGTCTCCAGAACACGGGCAGC

233

Qy454

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Db234

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Qy514

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Db294

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Qy574

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Db354

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Qy634

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693

Db414

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Qy694

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753

Db474

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533

Qy754

GTGATGGTCCTAAATAGCATGAGTGTGAGCTGGAGCGCCGGATCCAGATTTTCTTAACC

813

Db534

GTGATGGTCCTAAATAGCATGAGTGTGAGCTGGAGCGCCGGATCCAGATTTTCTTAACC

593

Qy814

TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATTA

873

Db594

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653

Qy874

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933

Db654

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713

Qy934

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993

Db714

CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTGTT

773

Qy994

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1053

Db774

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833

Qy1054

ATTGTCACCATTGGCTATGTGCTGACAAATGTGGCCCTACTTTACGACCATTAAATGCTGAG

1113

RESULT 13

US-10-163-866-33

; Sequence 33, Application US/10163866

; Publication No. US20030027188A1

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: SLCTs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-080C

; CURRENT APPLICATION NUMBER: US/10/163,866

Db 834 ATTGTCACCATGGCTATGTGCTGACAAATGTGGCCTACTTTACGACCAATTAATGCTGAG 893

QY 1114 GAGCTGCTGCTTCAAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 1173

Db 894 GAGCTGCTGCTTCAAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC 953

QY 1174 TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1233

Db 954 TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1013

QY 1234 TTTGCTGCTCAGGTTATTCTATGTTGCGTCTCGAGGGTCACTTCCAGAAATCCTC 1293

Db 1014 TTTGCTGCTCAGGTTATTCTATGTTGCGTCTCGAGGGTCACTTCCAGAAATCCTC 1073

QY 1294 TCCATGATTCATGTCGCAAGCACACTCCTCFACAGCTGTTATTGTTTGCACCCCTTG 1353

Db 1074 TCCATGATTCATGTCGCAAGCACACTCCTCFACAGCTGTTATTGTTTGCACCCCTTG 1133

QY 1354 ACAATGATAATGCTCTCTCTGGAGACCTCGACAGTCTTTTGAAATTCCTCAGTTTGCC 1413

Db 1134 ACAATGATAATGCTCTCTCTGGAGACCTCGACAGTCTTTTGAAATTCCTCAGTTTGCC 1193

QY 1414 AGGTGGCTTTTATTGGGCTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCA 1473

Db 1194 AGGTGGCTTTTATTGGGCTGGCAGTTGCTGGCTGATTTATCTTCGATACAAATGCCA 1253

QY 1474 GATATGCATCGTCCTTTCAAGTGCCACTGTTCCATCCAGCTTTGTTTCCCTTCACATGC 1533

Db 1254 GATATGCATCGTCCTTTCAAGTGCCACTGTTCCATCCAGCTTTGTTTCCCTTCACATGC 1313

QY 1534 CTCTTCATGTTGCCCTTTCCCTCTATTCCGACCCATTAGTACAGGGAATGGCTTCGTC 1593

Db 1314 CTCTTCATGTTGCCCTTTCCCTCTATTCCGACCCATTAGTACAGGGAATGGCTTCGTC 1373

QY 1594 ATCACTCTGACTGGAGTCCCTCGGTATTATCTCTTTATATATGSGACAAGAACCCAGG 1653

Db 1374 ATCACTCTGACTGGAGTCCCTCGGTATTATCTCTTTATATATGSGACAAGAACCCAGG 1433

QY 1654 TGGTTAGATAAATGTCAGAGAAAATACAGAACATTACAAATAATACTGGAAGTTGTA 1713

Db 1434 TGGTTAGATAAATGTCAGAGAAAATACAGAACATTACAAATAATACTGGAAGTTGTA 1493

QY 1714 CCAGAAGAGATAAGTTATGAACCTAATGGACTTGAGATCT 1753

Db 1494 CCAGAAGAGATAAGTTATGAACCTAATGGACTTGAGATCT 1533

RESULT 14

US-10-163-866-34

; Sequence 34, Application US/10163866

; Publication No. US20030027188A1

; GENERAL INFORMATION:

; APPLICANT: EXELIXIS, INC.

; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

; FILE REFERENCE: EX02-080C

; CURRENT APPLICATION NUMBER: US/10/163,866

; CURRENT FILING DATE: 2002-06-05

; PRIOR APPLICATION NUMBER: US 60/296,076

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/338,733

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/357,253

; PRIOR FILING DATE: 2002-02-15

; PRIOR APPLICATION NUMBER: US 60/357,600

; PRIOR FILING DATE: 2002-02-15

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34

; LENGTH: 2000

; TYPE: DNA

* ORGANISM: Homo sapiens

US-10-163-866-34

Query Match 59.8%; Score 1339; DB 14; Length 2000;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGC 393

Db 241 GAGAAAGTGCAGCTGAAGAGGAAAGTCACTTTACTGAGGGAGTCTCCATTATCATTTGC 300

QY 394 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTTAAGGGCGTCTCCAGAACACGGGCAGC 453

Db 301 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCCTTAAGGGCGTCTCCAGAACACGGGCAGC 360

QY 454 GTGGGCATGCTCTGTGACCATCTGTGACGGTGTGTGGGTCCTGTCACTATTTTGGAGCTTTG 513

Db 361 GTGGGCATGCTCTGTGACCATCTGTGACGGTGTGTGGGTCCTGTCACTATTTTGGAGCTTTG 420

QY 514 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 573

Db 421 TCTTATGCTGAATTGGGAACAACTATAAAGAAATCTGGAGGTCATTACACATATATTTG 480

QY 574 GAAGTCTTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATATAACGC 633

Db 481 GAAGTCTTTTGGTCCATTACAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATATAACGC 540

QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCATTTT 693

Db 541 CCTGCAGCTACTGCTGTGATATCCCTGGCATTTGGACGCTACATTTCTGGAACCATTTT 600

QY 694 ATTCAATGTGAAATCCCTGAACTTCCGATCAAGCTCAATACAGCTGTGGGCATAAATGTA 753

Db 601 ATTCAATGTGAAATCCCTGAACTTCCGATCAAGCTCAATACAGCTGTGGGCATAAATGTA 660

QY 754 GTGATGGTCTCTAAATAGCATGAGTGTGAGTGGAGCCCGGATCCAGATTTTCTTAAAC 813

Db 661 GTGATGGTCTCTAAATAGCATGAGTGTGAGTGGAGCCCGGATCCAGATTTTCTTAAAC 720

QY 814 TTTTGAAGCTCACAGCAATTTCTGATAATTTATAGTCCCTGGAGTTATGCAGCTAAATAAA 873

Db 721 TTTTGAAGCTCACAGCAATTTCTGATAATTTATAGTCCCTGGAGTTATGCAGCTAAATAAA 780

QY 874 GGTCAAAACGCAGAACTTTTAAAGACGCCTTTTACGGAAGAGATTCAGATATTACGGGTTG 933

Db 781 GGTCAAAACGCAGAACTTTTAAAGACGCCTTTTACGGAAGAGATTCAGATATTACGGGTTG 840

QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTGTT 993

Db 841 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTTGTT 900

QY 994 ACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTCCTTCCATATGTATATCCATGGCC 1053

Db 901 ACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTCCTTCCATATGTATATCCATGGCC 960

QY 1054 ATTGTCAACCATTTGGCTATGTCTGACAAATGTGGCTTACTTTACGACCATTAATGCTGAG 1113

Db 961 ATTGTCAACCATTTGGCTATGTCTGACAAATGTGGCTTACTTTACGACCATTAATGCTGAG 1020

QY 1114 GAGCTGCTGCTTTTCAAAATGCAGTGGCAGTACCTTTTCTGAGCGGCTACTGGGAAATTTT 1173

Db 1021 GAGCTGCTGCTTTTCAAAATGCAGTGGCAGTACCTTTTCTGAGCGGCTACTGGGAAATTTT 1080

QY 1174 TCATTAGCAGTTCAGATCTTTTGTGGCTTCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1233

Db 1081 TCATTAGCAGTTCAGATCTTTTGTGGCTTCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTG 1140

QY 1234 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1293

Db 1141 TTTGCTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCACTTCCAGAAATCCTC 1200

QY 1294 TCCATGATTCAATGTCGCAAGCACACTCCTCTACAGAGTGTATTGTTTTCACCCCTTTG 1353

Db 1201 TCCATGATTCAATGTCGCAAGCACACTCCTCTACAGAGTGTATTGTTTTCACCCCTTTG 1260

QY	1354	ACAATGATAATGCTCTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCCTCAGTTTGGC	1413
DB	1261	ACAATGATAATGCTCTCTCTGGAGACCTCGACAGTCTTTTGAATTTCCCTCAGTTTGGC	1320
QY	1414	AGGTGGCTTTTATTGGCTGGCAGTTGCTGGGCTGATTATCTTCGATACAAATGCCCA	1473
DB	1321	AGGTGGCTTTTATTGGCTGGCAGTTGCTGGGCTGATTATCTTCGATACAAATGCCCA	1380
QY	1474	GATATGCATCGTCCCTTCAAGGTGCCACGTGTTTCATCCAGCTTTGTTTTCTTCACATGC	1533
DB	1381	GATATGCATCGTCCCTTCAAGGTGCCACGTGTTTCATCCAGCTTTGTTTTCTTCACATGC	1440
QY	1534	CTCTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCATTAGTACAGGGAATGGCTTCGTC	1593
DB	1441	CTCTTCATGGTTGCCCTTTCCCTCTATTTCGGACCCATTAGTACAGGGAATGGCTTCGTC	1500
QY	1594	ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGGGACAGAAACCCAGG	1653
DB	1501	ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTTATTATATGGGACAGAAACCCAGG	1560
QY	1654	TGGTTTAGAATAATGTCAG	1672
DB	1561	TGGTTTAGAATAATGTCAG	1579

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RESULT 15
US-10-163-866-52
; Sequence 52, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-163-866-52

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	Query Match	58.0%;	Score 1299;	DB 14;	Length 1528;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 1399;	Conservative	0;	Mismatches	2; Indels 0; Gaps 0;
QY	334	GAGAAAGTGCAGCTGAAGAGGAAAGTCAC	TTTACTGAGGGGAGTCTCCATTATCAT	TGGC	3933
Db	128	GAGAAAGTGCAGCTGAAGAGGAAAGTCAC	TTTACTGAGGGGAGTCTCCATTATCAT	TGGC	187
QY	394	ACCATCATTTGGAGCAGGAATCTTCATCTCT	CCTAAGGGCGTGCTCCAGAAACACGGGCAGC		453
Db	188	ACCATCATTTGGAGCAGGAATCTTCATCTCT	CCTAAGGGCGTGCTCCAGAAACACGGGCAGC		247
QY	454	GTGGGCATGTCTCTGACCATCTGGACGGTGT	GTGGGGTCCCTGTCACTATTTGGAGCTTTG		513
Db	248	GTGGGCATGTCTCTGACCATCTGGACGGTGT	GTGGGGTCCCTGTCACTATTTGGAGCTTTG		307
QY	514	TCTTATGCTGAATTGGGAACAACATATAAGAA	ATCTGGAGGTCAATACACATATATTTTG		573
Db	308	TCTTATGCTGAATTGGGAACAACATATAAGAA	ATCTGGAGGTCAATACACATATATTTTG		367

QY	574	GAAGTCTTTGGTCCATTAC	CAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAAATACGC	633
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	368	GAAGTCTTTGGTCCATTAC	CAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATAAATACGC	427
QY	634	CTTGCACTACTGCTGTGATATCCCTGGCAATTTGGACGCTACATTTCTGGAAACCATTTTT	693	
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	428	CTTGCACTACTGCTGTGATATCCCTGGCAATTTGGACGCTACATTTCTGGAAACCATTTTT	487	
QY	694	ATTCAATGTGAAATCCCTGAACTTGGCAATCAAGCTCATTACAGCTGTGGSCATAACTGTA	753	
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	488	ATTCAATGTGAAATCCCTGAACTTGGCAATCAAGCTCATTACAGCTGTGGSCATAACTGTA	547	
QY	754	GTGATGGTCCCTAAATAGCATGAGTGTGAGCTGGAGCGCCCGGATCCAGATTTCTTTAAACC	813	
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	548	GTGATGGTCCCTAAATAGCATGAGTGTGAGCTGGAGCGCCCGGATCCAGATTTCTTTAAACC	607	
QY	814	TTTTGCAAGCTCACAGCAATTTCTGATAATATATAGTCCCTGGAGTTATGCAGCTAAATAAA	873	
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	608	TTTTGCAAGCTCACAGCAATTTCTGATAATATATAGTCCCTGGAGTTATGCAGCTAAATAAA	667	
QY	874	GGTCAAAACGAGAACTTTAAAGACGCTTTTTCAGGAAGAGATTTCAAGTATTACGGCGTTG	933	
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QY	934	CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTTACCTCAACTTTGTT	993	
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QY	994	ACTGAAGAACTAGAAAAACCCCTGAAAAAACCACTTCCCTTGCATAATATGTATATCCATGGCC	1053	
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QY	1054	ATTGTCACCAATGGCTATGTGCTGACAAATGTGGCCCTACTTTACGACCAATTAATGCTGAG	1113	
Db				
	848	ATTGTCACCAATGGCTATGTGCTGACAAATGTGGCCCTACTTTACGACCAATTAATGCTGAG	907	
QY	1114	GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTC	1173	
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QY	1174	TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTTGGCTCCATGAACGGTGGTG	1233	
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	1028	TTTGCTGTCTCAGGTTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCCAGAAATCCTC	1087	
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Db |||||
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Search completed: October 30, 2003, 10:16:49
Job time : 462 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 31, 2003, 11:39:24 ; Search time 39 Seconds
(without alignments)
4858.154 Million cell updates/sec

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Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	12	1.6	511	2	US-09-073-362-1	Sequence 1, Appli
2	12	1.6	511	2	US-09-243-920-1	Sequence 1, Appli
3	8	1.1	67	4	US-09-732-210-157	Sequence 157, App
C 4	8	1.1	241	4	US-09-071-035-308	Sequence 308, App
C 5	8	1.1	275	4	US-09-071-035-306	Sequence 306, App
C 6	8	1.1	325	4	US-09-198-452A-405	Sequence 405, App
C 7	8	1.1	332	4	US-09-328-352-6531	Sequence 6531, Ap
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C 10	8	1.1	585	4	US-09-107-532A-4126	Sequence 4126, Ap
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87	7	1.0	107	3	US-08-480-070C-16	Sequence 16, Appl
88	7	1.0	107	3	US-08-829-525-16	Sequence 16, Appl
89	7	1.0	107	3	US-08-609-583A-16	Sequence 16, Appl
90	7	1.0	107	3	US-09-177-249-145	Sequence 145, App
91	7	1.0	107	3	US-08-937-399-16	Sequence 16, Appl
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93	7	1.0	107	4	US-09-032-337-16	Sequence 16, Appl
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139	7	1.0	157	4	US-09-615-192A-341	Sequence 341, App
140	7	1.0	160	4	US-09-252-991A-23275	Sequence 23275, A
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154	7	1.0	241	2	US-08-825-781-4	Sequence 4, Appli
155	7	1.0	245	2	US-08-825-781-1	Sequence 1, Appli
156	7	1.0	246	4	US-09-328-352-5872	Sequence 5872, Ap
157	7	1.0	254	4	US-09-252-991A-25445	Sequence 25445, A
158	7	1.0	258	4	US-09-252-991A-30969	Sequence 30969, A

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C 167	7	1.0	334	4	US-09-252-991A-27154	Sequence 27154, A
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175	7	1.0	353	2	US-08-896-365-6	Sequence 6, Appli
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C 179	7	1.0	366	4	US-09-252-991A-19058	Sequence 19058, A
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C 183	7	1.0	374	4	US-09-252-991A-22425	Sequence 22425, A
C 184	7	1.0	376	4	US-09-252-991A-28256	Sequence 28256, A
C 185	7	1.0	390	4	US-09-198-452A-254	Sequence 254, App
C 186	7	1.0	391	4	US-09-107-532A-4419	Sequence 4419, Ap
C 187	7	1.0	392	4	US-09-071-035-260	Sequence 260, App
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C 189	7	1.0	409	4	US-09-198-452A-554	Sequence 554, App
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191	7	1.0	418	3	US-09-030-267-5	Sequence 5, Appli
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C 193	7	1.0	435	4	US-09-252-991A-17254	Sequence 17254, A
C 194	7	1.0	437	4	US-09-252-991A-17213	Sequence 17213, A
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C 229	7	1.0	555	4	US-09-252-991A-24056	Sequence 24056, A
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C 231	7	1.0	566	3	US-09-232-468A-22	Sequence 22, Appl

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150	3	US-08-857-076-17	Sequence 17, Appl
150	4	US-09-252-991A-25701	Sequence 25701, A
150	4	US-09-252-991A-26134	Sequence 26134, A
150	4	US-09-252-991A-30419	Sequence 30419, A
151	4	US-09-381-488-7	Sequence 7, Appli
151	4	US-09-252-991A-28890	Sequence 28890, A
152	4	US-09-316-081-2	Sequence 2, Appli
152	4	US-09-578-458-2	Sequence 2, Appli
152	4	US-09-578-458-18	Sequence 18, Appl
152	4	US-09-522-964A-2	Sequence 2, Appli
152	4	US-09-252-991A-18069	Sequence 18069, A
152	4	US-09-252-991A-32595	Sequence 32595, A
153	4	US-09-252-991A-18736	Sequence 18736, A
153	4	US-09-252-991A-32617	Sequence 32617, A
154	4	US-09-252-991A-23167	Sequence 23167, A
155	4	US-09-134-001C-4770	Sequence 4770, Ap
155	4	US-09-800-170-54	Sequence 54, Appl
155	4	US-09-732-210-1240	Sequence 1240, Ap
155	4	US-09-732-210-1249	Sequence 1249, Ap
155	4	US-09-107-532A-7084	Sequence 7084, Ap
156	3	US-09-142-583A-11	Sequence 11, Appl
156	4	US-08-467-602-381	Sequence 381, App
156	4	US-09-252-991A-17431	Sequence 17431, A
156	4	US-09-252-991A-24344	Sequence 24344, A
156	4	US-09-252-991A-28892	Sequence 28892, A
157	4	US-09-252-991A-17554	Sequence 17554, A
157	4	US-09-252-991A-22516	Sequence 22516, A
157	4	US-09-252-991A-30611	Sequence 30611, A
158	4	US-09-004-838-18	Sequence 18, Appl
158	4	US-09-134-001C-5378	Sequence 5378, Ap
158	4	US-09-134-001C-5407	Sequence 5407, Ap
158	4	US-09-252-991A-32537	Sequence 32537, A
159	1	US-07-732-242C-4	Sequence 4, Appli
159	3	US-08-993-165-7	Sequence 7, Appli
159	3	US-08-992-176-6	Sequence 6, Appli
159	4	US-09-540-448-7	Sequence 7, Appli
159	4	US-09-243-640-5	Sequence 5, Appli

962 6 0.8 159 4 US-08-929-847-7
C 963 6 0.8 159 4 US-09-252-991A-20158
964 6 0.8 159 4 US-09-252-991A-21119
C 965 6 0.8 159 4 US-09-252-991A-26017
C 966 6 0.8 159 4 US-09-252-991A-31393
C 967 6 0.8 159 4 US-09-732-210-734
968 6 0.8 159 4 US-09-107-532A-6407
C 969 6 0.8 159 6 5208144-35
970 6 0.8 160 2 US-08-162-402B-15
971 6 0.8 160 4 US-09-194-146-8
972 6 0.8 160 4 US-09-331-793-9
C 973 6 0.8 160 4 US-09-690-454-73
974 6 0.8 160 4 US-09-252-991A-21803
975 6 0.8 160 4 US-09-252-991A-31925
976 6 0.8 160 4 US-09-668-673B-7
977 6 0.8 160 4 US-09-328-352-6929
978 6 0.8 160 4 US-09-107-532A-3836
979 6 0.8 161 1 US-08-096-277-18
980 6 0.8 161 2 US-08-550-815-18
981 6 0.8 161 3 US-08-703-089-18
982 6 0.8 161 4 US-09-443-041A-6
983 6 0.8 161 4 US-09-252-991A-23969
984 6 0.8 161 4 US-09-252-991A-31686
C 985 6 0.8 161 4 US-09-328-352-6111
C 986 6 0.8 162 1 US-08-586-640-2
987 6 0.8 162 3 US-08-842-947-8
988 6 0.8 162 4 US-09-437-585-8
C 989 6 0.8 162 4 US-09-252-991A-20676
C 990 6 0.8 162 4 US-09-252-991A-22323
991 6 0.8 162 4 US-09-252-991A-32591
992 6 0.8 162 4 US-09-198-452A-948
C 993 6 0.8 163 1 US-08-075-545-1
C 994 6 0.8 163 1 US-08-256-261-17
995 6 0.8 163 2 US-09-066-074-2
996 6 0.8 163 2 US-08-555-912A-2
C 997 6 0.8 163 3 US-08-852-299-17
998 6 0.8 163 3 US-09-208-804-4
999 6 0.8 163 3 US-08-801-743-4
C1000 6 0.8 163 3 US-08-904-489-1

ALIGNMENTS

RESULT 1
US-09-073-362-1
; Sequence 1, Application US/09073362
; Patent No. 5942399
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

Sequence 7, Appli
Sequence 20158, A
Sequence 21119, A
Sequence 26017, A
Sequence 31393, A
Sequence 734, App
Sequence 6407, Ap
Patent No. 5208144
Sequence 15, Appl
Sequence 8, Appl
Sequence 9, Appl
Sequence 73, Appl
Sequence 21803, A
Sequence 31925, A
Sequence 7, Appl
Sequence 6929, Ap
Sequence 3836, Ap
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 6, Appl
Sequence 23969, A
Sequence 31686, A
Sequence 6111, Ap
Sequence 2, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 20676, A
Sequence 22323, A
Sequence 32591, A
Sequence 948, App
Sequence 1, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 1, Appl

; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
US-09-073-362-1

Alignment Scores:
Pred. No.: 0.00317 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-073-362-1 (1-511)

QY 517 TATGCTGAATTGGGAACAACACTATAAAGAAATCTGGA 552
|||||
Db 90 TyrAlaGluLeuGlyThrThrileLysLysSerGly 101

RESULT 2
US-09-243-920-1
; Sequence 1, Application US/09243920
; Patent No. 5981242
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,920
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/073,362
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ESOGTUT02
; CLONE: 2667831
US-09-243-920-1
Alignment Scores:
Pred. No.: 0.00317 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-243-920-1 (1-511)
QY 517 TATGCTGAATTGGGAACAACTATAAAGAAATCTGGA 552
Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101

RESULT 3
US-09-732-210-157
; Sequence 157, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 157
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-09-732-210-157
Alignment Scores:
Pred. No.: 36.4 Length: 67
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-732-210-157 (1-67)
QY 77 GAAAGAAAGAAAAGAGAGAGAGG 100
Db 43 GluArgLysLysLysArgGluArg 50

RESULT 4
US-09-071-035-308
; Sequence 308, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
```

```

; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 308:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-308
Alignment Scores:
Pred. No.: 31.3 Length: 241
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-071-035-308 (1-241)
QY 437 AGCAGCGCCTTAGGAGAGATGAAG 414
Db 96 SerThrProLeuGlyGluMetLys 103

RESULT 5
US-09-071-035-306
; Sequence 306, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
```


; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-306

Alignment Scores:
Pred. No.: 30.8 Length: 275
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-071-035-306 (1-275)

OY 437 AGCAGCGCCCTTAGGAGAGATGAAG 414
Db 125 SerThrProLeuGlyGluMetLys 132

RESULT 6

US-09-198-452A-405
; Sequence 405, Application US/09198452A
; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 405

; LENGTH: 325

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; FEATURE:

; NAME/KEY: SITE

; LOCATION: 1...325

; OTHER INFORMATION: Xaa=unknown or other

US-09-198-452A-405

Alignment Scores:
Pred. No.: 30.2 Length: 325
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-198-452A-405 (1-325)

OY 380 GAGACTCCCTCAGTAAAGTGACT 357
Db 149 GluThrProLeuSerLysValThr 156

RESULT 7

US-09-328-352-6531

; Sequence 6531, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6531
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6531

Alignment Scores:
Pred. No.: 30.1 Length: 332
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-328-352-6531 (1-332)

OY 1717 CTGGTACACTTCCAGTATTATT 1694
Db 30 LeuValGlnLeuProValLeuPhe 37

RESULT 8

US-09-073-362-3

; Sequence 3, Application US/09073362

; Patent No. 5942399

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Yue, Henry

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/073,362

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0514 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 515 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1665759

US-09-073-362-3

Alignment Scores:

Pred. No.: 28.6 Length: 515
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-073-362-3 (1-515)

QY 517 TATGCTGAATTGGGAACAATA 540
|||||

Db 98 TyrAlaGluLeuGlyThrThrIle 105

RESULT 9

US-09-243-920-3
; Sequence 3, Application US/09243920
; Patent No. 5981242
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/243,920
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/073,362
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0514 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1665759

US-09-243-920-3

Alignment Scores:
Pred. No.: 28.6 Length: 515
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 2 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-243-920-3 (1-515)

QY 517 TATGCTGAATTGGGAACAATA 540
|||||

Db 98 TyrAlaGluLeuGlyThrThrIle 105

RESULT 10

US-09-107-532A-4126
; Sequence 4126, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GIC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...585
; SEQUENCE DESCRIPTION: SEQ ID NO: 4126:
US-09-107-532A-4126

Alignment Scores:
Pred. No.: 28.2 Length: 585
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-107-532A-4126 (1-585)

QY 90 TTTTCTTTCTTTCTTTTTCCTT 67
|||||

Db 175 PhePheLeuSerPhePheLeu 182

RESULT 11

US-09-252-991A-19955
; Sequence 19955, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19955
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19955

Alignment Scores:
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US-09-667-170A-440 (1-2239) x US-09-252-991A-19955 (1-613)

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RESULT 12
US-09-012-710-11
; Sequence 11, Application US/09012710
; Patent No. 6087478
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.09% Indels: 0
DB: 4 Gaps: 0

; HYPOTHETICAL: NO
US-09-012-710-11
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US-09-667-170A-440 (1-2239) x US-09-012-710-11 (1-786)

Qy 766 AATAGCATGAGTGTCTCAGCTGGAGC 789
Db 549 AsnSerMetSerValSerTrpSer 556

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; Patent No. 6312887
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 786 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-556-273-11

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Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
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US-09-667-170A-440 (1-2239) x US-09-556-273-11 (1-786)

QY 766 AATAGCATGAGTGTCTCAGCTGGAGC 789
Db 549 AsnSerMetSerValSerTrpSer 556

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; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,710
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-012-710-10
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Db 549 AsnSerMetSerValSerTrpSer 556

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; Patent No. 6312887
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe

; APPLICANT: Moarefi, Ismail
; APPLICANT: Darnell, Jr., James E.
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
; TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,273
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,710
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-194
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

US-09-556-273-10
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US-09-667-170A-440 (1-2239) x US-09-556-273-10 (1-793)
QY 766 AATAGCATGAGTGTCTCAGCTGGAGC 789
Db 549 AsnSerMetSerValSerTrpSer 556

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
US-10-163-866-48
; Sequence 48, Application US/10163866
; Publication No. US20030027188A1
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; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
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; ORGANISM: Homo sapiens
US-10-163-866-48

Alignment Scores:
Pred. No.: 0 Length: 501
Score: 466.00 Matches: 466
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.66% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-48 (1-501)

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QY 514 TCTTATGTGAATTGGGAACAACACTATAAGAAATCTCGAGGTCAATTGGAGGTCAATACACATATTTTG 573
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QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGTCTGGCTGGTGGTTTACCTCAACTTTGTT 993
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Db 236 ProLeuAlaPheTyrTyrGlyMetTyrAlaTyrAlaGlyTrpPheTyrLeuAsnPheVal 255

QY 994 ACTGAAGAAGTAGAAAACCCCTGAAAAAACCATTTCCCTTGCAATATGATATATCCATGGCC 1053
|||||
Db 256 ThrGluGluValGluAsnProGluLysThrIleProLeuAlaIleCysIleSerMetAla 275

QY 1054 ATTGTACCAATTGGCTATGTGTGACAAATGTGGCCTACTTTACGACCACTAATGCTGAG 1113
|||||
Db 276 IleValThrIleGlyTyrValLeuThrAsnValAlaTyrPheThrThrIleAsnAlaGlu 295

QY 1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTTC 1173

Db 296 GluLeuLeuSerAsnAlaValAlaValThrPheSerGluArgLeuLeuGlyAsnPhe 315
QY 1174 TCATTAGCAGTCCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTG 1233
Db 316 SerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGlyVal 335
QY 1234 TTTGCTGTCTCCAGGTTATTCTATGTTGGCTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
Db 336 PheAlaValSerArgLeuPheTyrValAlaSerArgGluGlyHisLeuProGluIleLeu 355
QY 1294 TCCATGATTCAATGTCGCGAAGCACACTCCTCTACCAGCTGTTATTGTTTGCACCCCTTTG 1353
Db 356 SerMetIleHisValArgLysHisThrProLeuProAlaValIleValLeuHisProLeu 375
QY 1354 ACAATGATAATGCTCTTCTCTGGAGACCTCGACAGTCTTTTGAAATTCCTCAGTTTGGC 1413
Db 376 ThrMetIleMetLeuPheSerGlyAspLeuAspSerLeuLeuAsnPheLeuSerPheAla 395
QY 1414 AGTGGCTTTTATTTGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCA 1473
Db 396 ArgTrpLeuPheIleGlyLeuAlaValAlaGlyLeuIleTyrLeuArgTyrLysCysPro 415
QY 1474 GATATGCATCGTCCTTTCAAGGTGCCACTGTTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
Db 416 AspMetHisArgProPheLysValProLeuPheIleProAlaLeuPheSerPheThrCys 435
QY 1534 CTCTTCATGTTGCCCTTTCCCTCTATTCGGACCCATTTAGTACAGGATTGGCTTCGTC 1593
Db 436 LeuPheMetValAlaLeuSerLeuTyrSerAspPropheSerThrGlyIleGlyPheVal 455
QY 1594 ATCACTCTGACTGGAGTCCCTGCGGATTAATCTCTTTATTATATGGGACAAGAAACCCAGG 1653
Db 456 IleThrLeuThrGlyValProAlaTyrTyrLeuPheIleIleTrpAspLysLysProArg 475
QY 1654 TGGTTTAGAATAATGTCAGAGAAATAAACAGAACATTACAAATAACTGGAAGTTGTA 1713
Db 476 TrpPheArgIleMetSerGluLysIleThrArgThrLeuGlnIleIleLeuGluValVal 495
QY 1714 CCAGAGAAGATAAGTTA 1731
Db 496 ProGluGluAspLysLeu 501

RESULT 2
US-10-163-866-49
; Sequence 49, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-49

Alignment Scores:
Pred. No.: 0 Length: 501

Score: 466.00 Matches: 466
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 63.66% Indels: 0
DB: 15 Gaps: 0
US-09-667-170A-440 (1-2239) x US-10-163-866-49 (1-501)
QY 334 GAGAAAGTCAGCTGAAGAGGAAAGTCACCTTTACTGAGGGAGTCTCCATTATCATTTGGC 393
Db 36 GluLysValGlnLeuLysArgLysValThrLeuLeuArgGlyValSerIleIleGly 55
QY 394 ACCATCATTTGGAGCAGGAATCTTTCATCTCTCTCTAAGGGCGCTGCTCCAGAACACGGGCAGC 453
Db 56 ThrIleIleGlyAlaGlyIlePheIleSerProLysGlyValLeuGlnAsnThrGlySer 75
QY 454 GTGGGCATGTCTCTGACCATCTGGACGGTGTGTGGGTCCTGTCACTATTTTGGAGCTTTG 513
Db 76 ValGlyMetSerLeuThrIleTrpThrValCysGlyValLeuSerLeuPheGlyAlaLeu 95
QY 514 TCTTATGCTGAATTGGGAACAACACTATAAAGAAATCTGGAGGTCATTACACATATATTTTG 573
Db 96 SerTyrAlaGluLeuGlyThrThrIleLysLysSerGlyGlyHisTyrThrTyrIleLeu 115
QY 574 GAAGTCTTTGGTCCATTACCAGCTTTTGTACGAGTCTGGGTGGAACTCCTCATATAACGC 633
Db 116 GluValPheGlyProLeuProAlaPheValArgValTrpValGluLeuLeuIleIleArg 135
QY 634 CCTGCAGCTACTGCTGTGATATCCCTGGCATTCTGGACGCTACATCTCGAACCATTTT 693
Db 136 ProAlaAlaThrAlaValIleSerLeuAlaPheGlyArgTyrIleLeuGluProPhePhe 155
QY 694 ATTCAATGTGAAATCCCTGAACTTGGCATCCCTGGCATTCTGGACGCTACATCTGGGCACTA 753
Db 156 IleGlnCysGluIleProGluLeuAlaIleLysLeuIleThrAlaValGlyIleThrVal 175
QY 754 GTGATGGTCCTAAATAGCATGAGTGTCAAGTCAAGTCAAGTTCAGCTGTGGGCATAACTGTA 813
Db 176 ValMetValLeuAsnSerMetSerValSerTrpSerAlaArgIleGlnIlePheLeuThr 195
QY 814 TTTTGCAAGCTCACAGCAATTCTGATAATTATAGTCCCTGGAGTTATGCAGCTAATAATAA 873
Db 196 PheCysLysLeuThrAlaIleLeuIleIleIleValProGlyValMetGlnLeuIleLys 215
QY 874 GGTCAAAACGCAGAACTTTAAAGACGCGCTTTTCAGGAAGAGATTCAAGTATTACGCGGTTG 933
Db 216 GlyGlnThrGlnAsnPheLysAspAlaPheSerGlyArgAspSerSerIleThrArgLeu 235
QY 934 CCACTGGCTTTTATTATGGAATGTATGCATATGCTGGCTGGTTTACCTCAACTTGT 993
Db 236 ProLeuAlaPheTyrTyrGlyMetTyrAlaTyrAlaGlyTrpPheTyrLeuAsnPheVal 255
QY 994 ACTGAAGAAGTAGAAAAACCCCTGAAAAAACCATTCCTCCCTTGCATATGTATATCCATGGCC 1053
Db 256 ThrGluGluValGluAsnProGluLysThrIleProLeuAlaIleCysIleSerMetAla 275
QY 1054 ATTGTCACCATTTGGCTATGTGCTGACAAATGTGGCTACTTTACGACCAATTAATGCTGAG 1113
Db 276 IleValThrIleGlyTyrValLeuThrAsnValAlaTyrPheThrThrIleAsnAlaGlu 295
QY 1114 GAGCTGCTGCTTTCAAATGCAGTGGCAGTGACCTTTTCTGAGCGGCTACTGGGAAATTTTC 1173
Db 296 GluLeuLeuLeuSerAsnAlaValAlaValThrPheSerGluArgLeuLeuGlyAsnPhe 315
QY 1174 TCATTAGCAGTTCGATCTTTGTTGCCCTCTCCTGCTTTGGCTCCATGAACGGTGGTGTG 1233
Db 316 SerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGlyVal 335
QY 1234 TTTGCTGTCTCCAGGTTATTCTATGTTGGTCTCGAGAGGGTCACCTTCCAGAAATCCTC 1293
Db 336 PheAlaValSerArgLeuPheTyrValAlaSerArgGluGlyHisLeuProGluIleLeu 355
QY 1294 TCCATGATTCAATGTCGCGAAGCACACTCCTCTACCAGCTGTTATTGTTTGCACCCCTTTG 1353

Db 356 SerMetIleHisValArgLysHisThrProLeuProAlaValIleValLeuHisProLeu 375
QY 1354 ACAATGATAATGCTCTCTCTGGAGACCTCGACAGCTCTTTTGAATTTCCCTCAGTTTGGC 1413
Db 376 ThrMetIleMetLeuPheSerGlyAspLeuAspSerLeuLeuAsnPheLeuSerPheAla 395
QY 1414 AGGTGGCTTTTATTTGGCTGGCAGTTGCTGGGCTGATTTATCTTCGATACAAATGCCCA 1473
Db 396 ArgTrpLeuPheIleGlyLeuAlaValAlaGlyLeuIleTyrLeuArgTyrLysCysPro 415
QY 1474 GATATGCATCGTCCCTTCAAGGTGCCACTGTTTCATCCCAGCTTTGTTTTCCTTCACATGC 1533
Db 416 AspMetHisArgProPheLysValProLeuPheIleProAlaLeuPheSerPheThrCys 435
QY 1534 CTCTTCATGGTTGCCCTTCCCTCTATTTCGACCCCATTTAGTACAGGATGGCTTCGTC 1593
Db 436 LeuPheMetValAlaLeuSerLeuTyrSerAspProPheSerThrGlyIleGlyPheVal 455
QY 1594 ATCACTCTGACTGGAGTCCCTGCGTATTATCTCTTATTATATGGGACAAGAAACCCAGG 1653
Db 456 IleThrLeuThrGlyValProAlaTyrTyrLeuPheIleIleTyrAspLysLysProArg 475
QY 1654 TGGTTTAGAATAATGTCAGAGAAAATAACCAACAACATTACAAATAATACTGGAAGTTGTA 1713
Db 476 TrpPheArgIleMetSerGluLysIleThrArgThrLeuGlnIleIleLeuGluValVal 495
QY 1714 CCAGAAGAAGATAAGTTA 1731
Db 496 ProGluGluAspLysLeu 501

RESULT 3

US-09-738-973-586
; Sequence 586, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Elliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 586
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-738-973-586

Alignment Scores:
Pred. No.: 5.93e-83 Length: 97
Score: 93.00 Matches: 93
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.70% Indels: 0
DB: 10 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-738-973-586 (1-97)

QY 2 GAGTTGAAGTGAGCAGAGATCATGCCAGCGCTGGGTGACAGTGAGACTCTGTCTCAAACA 61
|||||

Db 1 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 20
QY 62 GAATTAAGGAAAAAGAAAGAAAAAGAGAGAGAGGAAATTCAGGCCAATTGTGGC 121
Db 21 GluLeuArgLysLysGluArgLysLysArgGluArgLysPheGlnAlaAsnCysGly 40
QY 122 ATAGATTTTATCATATTCTGGATTTTGGATTCTTTTGTCTTCATCACTGGATTCAG 181
Db 41 IleAspPheIleIlePheTrpIlePheTrpIleLeuLeuPheSerHisHisTrpIleGln 60
QY 182 GAAAGCCTGTTGTGTCCACCAATCTCCAAAGAGGATTACCTGCAGGGAAAATGTTAACGGGA 241
Db 61 GluSerLeuLeuCysProProSerProLysGluValThrCysArgGluMetLeuThrGly 80
QY 242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGG 280
Db 81 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 93

RESULT 4

US-09-854-133-586
; Sequence 586, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:

; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 586
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-854-133-586

Alignment Scores:
Pred. No.: 5.93e-83 Length: 97
Score: 93.00 Matches: 93
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.70% Indels: 0
DB: 10 Gaps: 0

US-09-667-170A-440 (1-2239) x US-09-854-133-586 (1-97)

QY 2 GAGTTGAAGTGAGCAGAGATCATGCCAGCGCTGGGTGACAGTGAGACTCTGTCTCAAACA 61
Db 1 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 20

QY 62 GAATTAAGGAAAAAGAAAGAAAAAGAGAGAGGAAATTCAGGCCAATTGTGGC 121
Db 21 GluLeuArgLysLysGluArgLysLysArgGluArgLysPheGlnAlaAsnCysGly 40

QY 122 ATAGATTTTATCATATTCTGGATTTTGGATTCTTTTGTCTTCATCACTGGATTCAG 181
Db 41 IleAspPheIleIlePheTrpIlePheTrpIleLeuLeuPheSerHisHisTrpIleGln 60

QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGAGGTTACCTGCAGGAAATGTTAACGGGA 241
Db 61 GluSerLeuLeuCysProProSerProLysGluValThrCysArgGluMetLeuThrGly 80

QY 242 GGCTGCCTTCCCTGGGCAACAAGGAGCCACCTGGGCAGG 280
Db 81 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 93

RESULT 5

US-10-144-649A-586

; Sequence 586, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 586
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-649A-586

Alignment Scores:
Pred. No.: 5.93e-83 Length: 97
Score: 93.00 Matches: 93
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.70% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-144-649A-586 (1-97)

QY 2 GAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACA 61
Db 1 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 20
QY 62 GAATTAAGGAAAAAGAAAGAAAGAGAGAGAGAGAAATTCAGGCCAATTGTGGC 121
Db 21 GluLeuArgLysLysGluArgLysLysLysArgGluArgLysPheGlnAlaAsnCysGly 40
QY 122 ATAGATTTATCATATTCTGGATTTTGGATTCTTTTGGATTCTTTTCTCATCTGATTTCAG 181
Db 41 IleAspPheIleIlePheTrpIlePheTrpIleLeuLeuPheSerHisHisTrpIleGln 60
QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA 241
Db 61 GluSerLeuLeuCysProProSerProLysGluValThrCysArgGluMetLeuThrGly 80
QY 242 GGCTGCCTTCCTGGGCAACAAGGAGCCACCTGGGCAGG 280
Db 81 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 93

RESULT 6
US-10-144-649A-742
; Sequence 742, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 742
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-649A-742

Alignment Scores:
Pred. No.: 5.84e-83 Length: 114
Score: 93.00 Matches: 93
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12.70% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-144-649A-742 (1-114)

QY 2 GAGGTTGAAGTGAGCAGAGATCATGCCAGCCTGGGTGACAGTGAGACTCTGTCTCAAACA 61
Db 18 GluValGluValSerArgAspHisAlaSerLeuGlyAspSerGluThrLeuSerGlnThr 37
QY 62 GAATTAAGGAAAAAGAAAGAAAGAGAGAGAGAGAAATTCAGGCCAATTGTGGC 121
Db 38 GluLeuArgLysLysGluArgLysLysLysArgGluArgLysPheGlnAlaAsnCysGly 57
QY 122 ATAGATTTATCATATTCTGGATTTTGGATTCTTTTGGATTCTTTTCTCATCTGATTTCAG 181
Db 58 IleAspPheIleIlePheTrpIlePheTrpIleLeuLeuPheSerHisHisTrpIleGln 77
QY 182 GAAAGCCTGTTGTGTCCACCATCTCCAAAGGAGGTTACCTGCAGGAAATGTTAACGGGA 241
Db 78 GluSerLeuLeuCysProProSerProLysGluValThrCysArgGluMetLeuThrGly 97
QY 242 GGCTGCCTTCCTGGGCAACAAGGAGCCACCTGGGCAGG 280
Db 98 GlyCysLeuProTrpAlaThrArgSerHisLeuGlyArg 110

RESULT 7

US-10-214-867A-13
; Sequence 13, Application US/10214867A
; Publication No. US20030148444A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-214-867A-13

Alignment Scores:
Pred. No.: 2.36e-36 Length: 502
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.28% Indels: 0
DB: 12 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-214-867A-13 (1-502)

QY 1171 TTCTCATTAGCAGTTCGATCTTTTGGTTGGCCTCTCCTTGGCTCCATGACGGTGGT 1230
Db 315 PheSerLeuAlaValProIlePheValAlaLeuSerCysPheGlySerMetAsnGlyGly 334
QY 1231 GTGTTTGTCTCCAGGTTATTCTATGTTGCGTCTCGAGAGGGTCCACCTTCAGAAATC 1290
Db 335 ValPheAlaValSerArgLeuPheTyrValAlaSerArgGluGlyHisLeuProGluIle 354

QY	1291	CTCTCCATGATTCATGTC	1308
Db	355	LeuSerMetIleHisVal	360
RESULT 8			
US-09-738-973-587			
; Sequence 587, Application US/09738973			
; Patent No. US20020110563A1			
; GENERAL INFORMATION:			
; APPLICANT: Reed, Steven G.			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Fling, Steven P.			
; APPLICANT: Mohamath, Raodoh			
; APPLICANT: Algate, Paul A.			
; APPLICANT: Secrist, Heather			
; APPLICANT: Indirias, Carol Yoseph			
; APPLICANT: Benson, Darin R.			
; APPLICANT: Elliot, Mark			
; APPLICANT: Mannion, Jane			
; APPLICANT: Kalos, Michael D.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR			
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.475C9			
; CURRENT APPLICATION NUMBER: US/09/738,973			
; CURRENT FILING DATE: 2000-12-14			
; NUMBER OF SEQ ID NOS: 587			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 587			
; LENGTH: 16			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-738-973-587			
Alignment Scores:			
Pred. No.:	1.96e-06	Length:	16
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.19%	Indels:	0
DB:	10	Gaps:	0
US-09-667-170A-440 (1-2239) x US-09-738-973-587 (1-16)			
QY	104	TTCCAGGCCAATTGTGGCATAGATTTTATCATATTTCTGGATTTTGG	151
Db	1	PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp	16
RESULT 9			
US-09-854-133-587			
; Sequence 587, Application US/09854133			
; Publication No. US20020183499A1			
; GENERAL INFORMATION:			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Mohamath, Raodoh			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: Benson, Darin R.			
; APPLICANT: Secrist, Heather			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR			
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.475C10			
; CURRENT APPLICATION NUMBER: US/09/854,133			
; CURRENT FILING DATE: 2001-05-11			
; NUMBER OF SEQ ID NOS: 735			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 587			
; LENGTH: 16			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-854-133-587			
Alignment Scores:			
Pred. No.:	1.96e-06	Length:	16
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.19%	Indels:	0
DB:	10	Gaps:	0
US-09-667-170A-440 (1-2239) x US-09-738-973-587 (1-16)			
QY	104	TTCCAGGCCAATTGTGGCATAGATTTTATCATATTTCTGGATTTTGG	151
Db	1	PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp	16
RESULT 10			
US-10-144-649A-587			
; Sequence 587, Application US/10144649A			
; Publication No. US20030118599A1			
; GENERAL INFORMATION:			
; APPLICANT: Lodes, Michael J.			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Fan, Liqun			
; APPLICANT: Algate, Paul A.			
; APPLICANT: McNeill, Patricia D.			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR			
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121.475C11			
; CURRENT APPLICATION NUMBER: US/10/144,649A			
; CURRENT FILING DATE: 2002-08-21			
; NUMBER OF SEQ ID NOS: 749			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 587			
; LENGTH: 16			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-144-649A-587			
Alignment Scores:			
Pred. No.:	1.96e-06	Length:	16
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.19%	Indels:	0
DB:	15	Gaps:	0
US-09-667-170A-440 (1-2239) x US-10-144-649A-587 (1-16)			
QY	104	TTCCAGGCCAATTGTGGCATAGATTTTATCATATTTCTGGATTTTGG	151
Db	1	PheGlnAlaAsnCysGlyIleAspPheIleIlePheTrpIlePheTrp	16
RESULT 11			
US-10-029-386-32531			
; Sequence 32531, Application US/10029386			
; Publication No. US20030194704A1			
; GENERAL INFORMATION:			
; APPLICANT: Penn, Sharron G.			
; APPLICANT: Rank, David R.			
; APPLICANT: Hanzel, David K.			
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID			
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO			
; FILE REFERENCE: AEOMICA-X-2			
; CURRENT APPLICATION NUMBER: US/10/029,386			
; CURRENT FILING DATE: 2001-12-20			
; NUMBER OF SEQ ID NOS: 34288			
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1			
; SEQ ID NO 32531			
; LENGTH: 166			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: MAP TO AL135998.2			
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6			
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5			

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: Q9UM01, EVALUE 9.00e-83
US-10-029-386-32531

Alignment Scores:
Pred. No.: 0.0149 Length: 166
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 12 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-029-386-32531 (1-166)

QY 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552

Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101

RESULT 12

US-10-214-867A-11

; Sequence 11, Application US/10214867A
; Publication No. US2003014844A1
; GENERAL INFORMATION:
; APPLICANT: ENDOU, HITOSHI
; APPLICANT: KANAI, YOSHIKATSU
; TITLE OF INVENTION: SODIUM-INDEPENDENT SMALL NEUTRAL AMINO ACID
; TITLE OF INVENTION: TRANSPORTERS TRANSPORTING L- AND D-AMINO ACIDS AND
; TITLE OF INVENTION: GENES THEREOF
; FILE REFERENCE: 57783 (71526)
; CURRENT APPLICATION NUMBER: US/10/214,867A
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: PCT/JP01/00031
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: JP 2000-28822
; PRIOR FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-214-867A-11

Alignment Scores:
Pred. No.: 0.0134 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 12 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-214-867A-11 (1-511)

QY 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552

Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101

RESULT 13

US-10-163-866-41

; Sequence 41, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605

; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-41

Alignment Scores:

Pred. No.: 0.0134 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-41 (1-511)

QY 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552

Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101

RESULT 14

US-10-163-866-42

; Sequence 42, Application US/10163866
; Publication No. US20030027188A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SLC7s AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-080C
; CURRENT APPLICATION NUMBER: US/10/163,866
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-866-42

Alignment Scores:

Pred. No.: 0.0134 Length: 511
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.64% Indels: 0
DB: 15 Gaps: 0

US-09-667-170A-440 (1-2239) x US-10-163-866-42 (1-511)

QY 517 TATGCTGAATTGGGAACAACATAAAGAAATCTGGA 552

Db 90 TyrAlaGluLeuGlyThrThrIleLysLysSerGly 101

RESULT 15

US-09-815-923-16

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; Sequence 16, Application US/09815923
; Publication No. US20020197644A1
; GENERAL INFORMATION:
; APPLICANT: Gill, Sarjeet S.
; APPLICANT: Ross, Linda S.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Use of Insect Cell Membrane Transporters as No. US20020197644A1e1
; TITLE OF INVENTION: Target Sites for Insecticides
; FILE REFERENCE: 023070-093800US
; CURRENT APPLICATION NUMBER: US/09/815,923
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Aedes aegypti
; FEATURE:
; OTHER INFORMATION: LAT transporter
US-09-815-923-16
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Alignment Scores:
Pred. No.:      0.132      Length:      517
Score:          11.00      Matches:     11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      1.50%      Indels:    0
DB:               10        Gaps:      0
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US-09-667-170A-440 (1-2239) x US-09-815-923-16 (1-517)

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QY      409  GGAATCTTCATCTCTCTAAGGCGTGCTCCAG 441
Db       74  GlyIlePheIleSerProLysGlyValLeuGln 84
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Search completed: October 31, 2003, 12:25:22
Job time : 172 secs